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18	753.6	87.5	969	6	BD272516	Secreted

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23	752	87.3	1818	8	AY128643	AY128643	Homo sapi
24	752	87.3	4531	6	CS130842	CS130842	Sequence
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29	747.6	71.4	1379	9	BC036995	BC036995	Mus muscu
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35	546.4	63.5	61505	8	AF305426	AF305426	Homo sapi
36	546.4	63.5	130435	8	HS17837	AL035541	Human DNA
37	544.4	63.2	1583	6	AX593655	AX593655	Sequence
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40	460.6	53.5	1713	6	BD272517	BD272517	Secrated
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42	460.6	53.5	1713	6	BD272519	BD272519	Secrated
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LOCUS	AX392419
DEFINITION	Sequence 3 from Patent WO0216416.
ACCESSION	AX392419
VERSION	AX392419.1
KEYWORDS	GI:19700734
SOURCE	.
ORGANISM	Homo sapiens (human)
	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1  
AUTHORS  
Lee, R. T., Landschulz, K. T., Kennedy, S. P., Thompson, J. F. and

TITLE	Author
Diagnosis and treatment of cardiovascular conditions	Thari, T.G.

**JOURNAL**  
Patent: WO 0216418-A 3 28-FEB-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER INC. (US)

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Qy	781	CTCCACCCACACACATCGGGCGCCCTTAAGAGCGCGACCATCTGGAGCAAGAAGAGAT	840
Db	1193	CTCCACCCACACACATCGCGCCCTTAAGAGCGCGACCATCTGGAGCAAGAAGAGAT	1253
Qy	841	AAACAGAAAGACACCTCTC	861
Db	1253	AAACAGAAAGACACCTCTC	1273
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DEFINITION	Sequence 2 from Patent EP1471075.		linear
ACCESSION	CO894692		
VERSION	CO894692.1	GI:55467441	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1		
TITLE	Rosenthal, A.D., Pilarsky, C., Dahl, E., Specht, T., Bruemendorf, T., Lichtner, R., Stab, E., Roepcke, S. and Li, X. I.		
JOURNAL	Human nuclear acid sequences expressed in pancreatic carcinomas Patent: EP 1471075-A 2 27-OCT-2004; Hinemann, Bernd (DB); Rosenthal, Andrie (DE); Pilarsky, Christian (DE); Dahl, Edgar (DE); Specht, Thomas (DB); Lichtner, Rosemarie (DE)		
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Qy	61	TCCTGACGCTGCAACTGCAAAAGCTCTTTGTTCAAGAGCATGAGATCACGAGCTGGAG	120
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Qy	121	TTTGTTCAGATCATCATCATCTGTTGGTGGTGAATGATGATGATGATGATCATCTGC	180
Db	121	TTTGTTCAGATCATCATCATCTGTTGGTGGTGAATGATGATGATGATGATCATCTGC	180
Qy	181	CTGCTGAGGCACTACAGCTGTCTGACAGGTCCTTCATGACCGGACAGCCAGGGGGCGG	240
Db	181	CTGCTGAGGCACTACAGCTGTCTGACAGGTCCTTCATGACCGGACAGCCAGGGGGCGG	240
Qy	241	AGGAGAGAGATGACCTGTCTCAGAAAGATGCTGTGGCCCTCGAGAGCACAAGTCTCA	300
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Qy	301	GGCAACGGAATCCAGAGCTCGACAGGCTCTACGCCGCCCTTCGGCCACCGACCGCTGGCC	360
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Qy	361	GTGCGGCGCTTGGCGCCAGGGGAGGCGCTTCAACCGTTTCAGGCCACCTATCGTACCTG	420
Db	361	GTGCGGCGCTTGGCGCCAGGGGAGGCGCTTCAACCGTTTCAGGCCACCTATCGTACCTG	420

Oy	421	CAGACGAGATGCACTGCAACCCACCATTCTGCTGTCAACGCGGAGAGACCCCAACC	480
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Oy	601	AGGCTGGAGGAGCCCTGTCACCCCAAGCATCTCGGAGCATAGCGCCACAGTGTACCGC	660
Db	601	AGGCTGGAGGAGCCCTGTCACCCCAAGCATCTCGGAGCATAGCGCCACAGTGTACCGC	660
Oy	661	AGCGCGGAGGCGCATGAGAGGAGCGCGCGCCACCTACAGCGAGTCAATCGCACTAACCG	720
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Oy	721	GGGTCTCTCTTCCAGACCAAGCAGAGAGAGTGGCGCGCCCTCTTGCTGAGAGGAGCCCGG	780
Db	721	GGGTCTCTCTTCCAGACCAAGCAGAGAGAGTGGCGCGCCCTCTTGCTGAGAGGAGCCCGG	780
Oy	781	CTCCACGACACACATCGGCGCCCTTAGAGAGCGCACCATCTTGAGCAAGAGAGAT	840
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Oy	841	AAACAGAAAGACACCCCTTC	861
Db	841	AAACAGAAAGACACCCCTTC	861
RESULT 4			
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DEFINITION	Sequence 109 from Patent WO2004038020.	linear	PAT 24-MAY-2004
ACCESSION	COB12357		
VERSION	COB12357.1	GI:47601977	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Wittig,R., Poustka,A., Mollenhauer,J. and Schendendorf,D.		
AUTHORS	Target genes for the diagnosis and treatment of cancer		
TITLE	Patent: WO 2004038020-A 109 06-MAY-2004;		
JOURNAL	Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechte		
DE			
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Best Local Similarity	100.0%;	Pred. No. 1,1e-126;	Indels 0; Gaps 0;
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Oy	1	ATGACACCGCTTGATGGGGGTCAACAGACACGCGCGCGCGCGCGCGCGCGCGCAATGTC	60
Db	321	ATGACACCGCTTGATGGGGGTCAACAGACACGCGCGCGCGCGCGCGCGCGCAATGTC	380
Oy	61	TCTGCAAGTGCACATGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAGAGAGTGGAG	120
Db	381	TCTGCAAGTGCACATGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAGAGAGTGGAG	440



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Qy	422	CAGACACGAGATCGACCTGTCACACCCACCATCTCGCTGAGACGGGGAGAGACCCCCACACC	480
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Qy	481	TACCAAGAGCCCTGTGACCCCTTCAGCTTGGGAACCCCGAGCAGCAGCTTGAACTGAACCGG	540
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Qy	541	GAGTCGGTGGCGCGACCCCGCAAGAAACCAATCTTTCGACAGTGAACCTGATGATGATGCC	600
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Qy	721	GAGTCCTCTTTCACAGCACGACGAGAGCATGTGGCGCGCCTCTTCTGTGAGGGGACCCGG	780
Db	1041	GAGTCCTCTTTCACAGCACGACGAGAGCATGTGGCGCGCCTCTTCTGTGAGGGGACCCGG	1100
Qy	781	CTCCACACACACACATTCGGCGCCCTTAAGAGCGCAGCCATCTTGAGCCTAAAGAGAGGAT	840
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RESULT	8
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LOCUS	4839 bp mRNA linear PRI 21-OCT-2001
DEFINITION	Homo sapiens STAG1/PMEPAl mRNA, complete cds.
ACCESSION	AF305616
VERSION	AF305616.1 GI:16303741

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	

REFERENCE 1 (bases 1 to 4839)

AUTHORS	TITLE
Rae, F. K., Hooper, J. D., Nicol, D. L. and Clements, J. A.	Characterization of a novel gene, STAG1/PNEPAL, upregulated in

REFERENCE	JOURNAL	PUBMED
2 (Bases 1 to 4839)	Mol. Carcinog. 32 (1), 44-53 (2001)	11568975

**TITLE** Direct Submission  
**JOURNAL** Submitted (14-SEP-2000) Centre for Molecular Biotechnology, and

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Query Match	100.0%;	Score 861;	DB 8;	Length 4839;
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Matches 861;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Oy	781	CTCCACCAACACACATCGGCGCCCTTGAGAGCGCCACCTCGGAGCAAGAGAT	840
Db	1174	CTCCACCAACACACATCGGCGCCCTTGAGAGCGCCACCTCGGAGCAAGAGAT	1233
Oy	841	AAACGAAAGGACACCCCTCTC	861
Db	1234	AAACGAAAGGACACCCCTCTC	1254
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LOCUS			linear
AX775889			PAT 14-JUL-2003
DEFINITION	Sequence 159 from Patent WO03048202.		
ACCESSION	AX775889		
VERSION	AX775889.1		
KEYWORDS	GI:32693607		
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
JOURNAL	Momidae; Homo.		
FEATURES	1		
source	Matsuda, A. and Muramatsu, S.		
	NP-KB activating gene		
	Patent: WO 03048202-A, 159, 12-JUN-2003;		
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Db	381	TCCTGCACGTGCACCTGCAAAAGCTCTTTGTTCCAGACATGAGATCACGAGCTGGAG	440
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QY 841 AAACAGAAAGACACCTCTC 861
Db 1161 AAACAGAAAGACACCTCTC 1181

RESULT 11
LOCUS BC015918 1061 bp mRNA linear PRI 01-APR-2004
DEFINITION Homo sapiens transmembrane, prostate androgen induced RNA, mRNA
ACCESSION BC015918
VERSION BC015918
KEYWORDS (CDNA clone IMAGE:4559576), partial cds.
SOURCE BC015918.1 GI:16198474
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1061)
AUTHORS Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Abramson, R.D., Collins, P.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,
Diachenko, L., Marusina, K., Faxmer, A.A., Rubin, G.M., Hong, L.,
Stableton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Ueda, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loguella, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, T., Helton, B., Ketterman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

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TITLE
JOURNAL
PUBMED
AUTHORS
REFERENCES
JOURNAL
REMARK
COMMENT
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smailus, D.E.,
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 1061)
Strauberg, R.
Direct Submission
Submitted (15-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing By: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telka Olson, Diana Palquist, Anca Petrescu, Anna Lissa Prabh,
Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,
Dune Smalun, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAL Plate: 29 Row: e Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarly but not
identical to protein.
Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="NIH MGC_14"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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/note="synonyms: PMEPA1, STAG1"
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/db_xref="MIM:606564"
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/codon_start=2
/product="TMEPA1 protein"
/protein_id="AAH15918.2"
/db_xref="GI:4594653"
/db_xref="GeneID:56937"
/db_xref="MIM:606564"
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MMVVITCLLSHYLSRSFISRSQRRREDAUSSGCLPSSSTVSGNGIPBQV
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LRDEQQLNRRESVRAPPNRTIFSDILMSARIGCPSPSSSGSATCYGSGGM
EGPPTYSVETVGHVYGSFQHQSSGPPSLLEGTRTHHTIAPLESAAIMSKDKOK
GHP1."
323..541
/note="TMEPA1"
/feature="BCAS2; Region: Breast carcinoma amplified sequence
2 (BCAS2). This family consists of several eukaryotic
sequences of unknown function. The mammalian members of

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Qy	642	CAGCGCCA	CGTGTCTA	CGGCA	CGCGCGGCGCAT	TGAGAGGGGCGCGCGCCACCTTA	CAGCGA	701		
Db	542	CAGCCCA	CAGTGTCT	CGGCA	CGCGCGGCGCAT	TGAGAGGGGCGCGCGCCACCTTA	CAGCGA	601		
Qy	702	GGTCA	TCCGGCC	CACTAC	CCGGGGGTCC	CTTCCTTCC	CAGCAC	CGAGAGAGAGCAT	GTGGGCGCGCCCTC	761
Db	602	GGTCA	TCCGGCC	CACTAC	CCGGGGGTCC	CTTCCTTCC	CAGCAC	CGAGAGAGAGCAT	GTGGGCGCGCCCTC	661
Qy	762	CTTGTCTG	AGGGGAG	CCCGGCTC	CACACA	CA	CACACAT	TGGCGCCCTTA	GAGAGGGC	821
Db	662	CTTGTCTG	AGGGGAG	CCCGGCTC	CACACA	CA	CACACAT	TGGCGCCCTTA	GAGAGGGC	721
Qy	822	CTGGAG	CAAGAG	AGATTA	ACAGAA	AGGAC	ACCTCTC			861
Db	722	CTGGAG	CAAGAG	AGATTA	ACAGAA	AGGAC	ACCTCTC			761

RESULT 13					
AF224278	AF224278	1141 bp	mRNA	linear	PRI 18-JUL-2000
LOCUS					
DEFINITION	Homo sapiens PMPAL protein (PMPAL) mRNA,			complete cds.	
ACCESSION	AF224278				
VERSION	AF224278.1				
KEYWORDS	. GI:9255608				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1. (bases 1 to 1141)
AUTHORS	Xu,L.L., Shannugam,N., Segawa,T., Seesterhenn,I.A., McLeod,D.G., Moul,J.W. and Srivastava,S.
TITLE	A novel androgen-regulated gene, PMEPA1, located on chromosome 20q13 exhibits high level expression in prostate
JOURNAL	Genomics 66 (3), 257-263 (2000)
PUBMED	10873380
REFERENCE	2. (bases 1 to 1141)
AUTHORS	Xu,L.L., Shannugam,N., Segawa,T., Seesterhenn,I.A., McLeod,D.G., Moul,J.W. and Srivastava,S.
TITLE	Direct Submission
JOURNAL	Submitted (12-JAN-2000) CPDR, USHS, 1530 East Jefferson Street, Rockville, MD 20852, USA
FEATURES	Location/Qualifiers
source	1..1141

gene  
CDS

/gene="PMEPA1"  
/note="type 1b transmembrane protein; expression is induced in response to the synthetic androgen, R1881; expression is abundant in, and restricted to, prostate glandular epithelial cells, similar to the predicted protein encoded by sequence deposited at Genbank Accession Number NP 004329"

[illegible]

## ORIGIN

Query Match	87.6%	Score 754.2;	DB 8;	Length 1141;
Best Local Similarity	98.3%	Pred. No. 1e-109;		
Matches 762; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0;

QY	87	TTTGTTCAGAGCATGAGAGATCACGGAGCTGGAGATTGTTCAATCATCATCATTCGGGT	146
Db	77	TCTCTCTGGAAACGAGGCMAATGGGGAGCTGGAGATTGTTCAAGTATCATCATCTGGT	136
QY	147	GATGATGATGGTGAATGGTGGTGGTGAATCACTGGCTCTGAGCCACTACAAGCTGTCTGC	206
Db	137	GATATGATGATGATGGTGGTGGTGAATCACTGGCTCTGAGCCACTACAAGCTGTCTGC	196
QY	207	ACGGTCTTCATCAGCCGGGCAAGCCAGGGCGGAGAGAGAGATGCTCTGTCTTCAGA	266
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QY	267	AGGATGCTGTGGGCTCTTCGAGAGACAAGTGTCAAGGCMAACGGATTCCTCAGACCGGAGT	326
Db	257	AGGATGCTGTGGGCTCTTCGAGAGACAAGTGTCAAGGCMAACGGATTCCTCAGACCGAGT	316
QY	327	CTAGGCCCCGGCTGGGCCCAACGACCGGCTGGCGCGGCTCTTCGCCCCAGCGGAGCG	386
Db	317	CTAGGCCCCGGCTGGGCCCAACGACCGGCTGGCGCGGCTCTTCGCCCCAGCGGAGCG	376
QY	387	CTTCACACGCTTCAGAGCCACTATCCGTACTTCGACAGACGAGATTCGACTTCGACCCAC	446
Db	377	CTTCACACGCTTCAGAGCCACTATCCGTACTTCGACAGACGAGATTCGACTTCGACCCAC	436
QY	447	CATCTCGCTGTCAAGCGGGAGAGAGCCGCCACTTACAGGGCCCCCTGCAACCTCTCAGCT	506
Db	437	CATCTCGCTGTCAAGCGGGAGAGAGCCGCCACTTACAGGGCCCCCTGCAACCTCTCAGCT	496
QY	507	TCGGGACCCCGAGCGAGCTGGAACTGAAACCGGAGATCGGTGCGGCAACCCCAACAG	566
Db	497	TCGGGACCCCGAGCGAGCTGGAACTGAAACCGGAGATCGGTGCGGCAACCCCAACAG	556
QY	567	AACCATCTTCGACAGTGAACCTGATGATGATGTCAGAGCTGGGCGGACCCCTGCCCCAG	626
Db	557	AACCATCTTCGACAGTGAACCTGATGATGATGTCAGAGCTGGGCGGACCCCTGCCCCAG	616
QY	627	CAGTAACTCGGGCATCAGCGCCACGTGTAAAGGCAAGCGCGGGGCGCATGAGAGGGGCGGC	686
Db	617	CAGTAACTCGGGCATCAGCGCCACGTGTAAAGGCAAGCGCGGGGCGCATGAGAGGGGCGGC	676
QY	687	GCCCACTCAAGCGAGATCATCGGCACTACCGGGGCTCTCTTCCAGCACAGCAGAG	746
Db	677	GCCCACTCAAGCGAGATCATCGGCACTACCGGGGCTCTCTTCCAGCACAGCAGAG	736
QY	747	CAGTGGGCGGCTCTTGTGAGAGGGAGCCCGGCTCCACCAACAACATCGCGCCCT	806
Db	737	CAGTGGGCGGCTCTTGTGAGAGGGAGCCCGGCTCCACCAACAACATCGCGCCCT	796
QY	807	AGAGAGCCGACGCTATGAGACCAAGAAAGAAAGATTAACAAAGAACCCCTTC	861
Db	797	AGAGAGCCGACGCTATGAGACCAAGAAAGAAAGATTAACAAAGAACCCCTTC	851

RESULT 14				
CS130841				
LOCUS	CS130841	4538 bp	DNA	linear
DEFINITION	Sequence 127 from Patent WO2005064009.			
ACCESSION	CS130841			
VERSION	CS130841.1	GI:71792911		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homidae; Homo.			
REFERENCE	1			
AUTHORS	Obermoltz, T.F.			
TITLE	Classification of cancer			
JOURNAL	Patent: WO 2005064009-A 127 14-JUL-2005;			



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Db      667 CAGTAAGTGGGATCAGGCCACGTCCTACGGCAGCGGCGGGCGCATGGAAGGGCCGCC 726
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Db      727 GCCCACTTACAGCGAGGTGATCGGCCACTAACCCGGGGTCTCTCTTCAGCACCAAGAGAG 786
Qy      747 CAGTGGGCGGCTCTTGTGTGAAGGGACCGGCTCCACACACACATGCGGCCCT 806
Db      787 CAGTGGGCGGCTCTTGTGTGAAGGGACCGGCTCCACACACACATGCGGCCCT 846
Qy      807 AGAGAGCGCAGCATCTGAGCAAGAAGATTAACAGAAAGACACCTCTC 861
Db      847 AGAGAGCGCAGCATCTGAGCAAGAAGATTAACAGAAAGACACCTCTC 901
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Search completed: February 28, 2006, 12:48:11  
Job time : 4613.99 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 08:23:08 ; Search time 586.364 Seconds  
(without alignments)  
9786.244 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861  
Sequence: 1 atgcacccgtgatgaggggggt.....aacagaaaggacaccccttc 861

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: N\_Geneseq\_21.\*
- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	100.0	864	11	ADN38809 Cancer/an
2	861	100.0	1321	6	ABK12137 Human CDN
3	861	100.0	4519	13	ADK97454 Pancreat
4	861	100.0	4839	8	ACC49552 Tumour-as
5	861	100.0	4839	11	ADP65809 Human STA
6	861	100.0	4839	11	ADP65729 Human tra
7	861	100.0	4839	12	ADM67045 Human hom
8	861	100.0	4839	13	ADR65875 Human pro
9	861	100.0	4839	13	ADR66778 Human pro
10	861	100.0	4839	13	ADU06063 Novel bro
11	861	100.0	4839	14	ADM43368
12	861	100.0	4911	13	ACN40804 Tumour-as
13	861	100.0	4930	14	AEH22787
14	859.4	99.8	1383	10	ADC37326 Nuclea
15	755.2	87.7	969	3	AAA75151 CDNA enco
16	754.2	87.6	1140	6	ABK92120 Prostate
17	754.2	87.6	1141	10	ADK75588 Prostate
18	754.2	87.6	1850	8	ACC49536 Tumour-as
19	754.2	87.6	4527	11	ADL83313 Human and

20	754.2	87.6	4527	14	ADV85880 Human ARP
21	754.2	87.6	4538	14	AEB22832 Human col
22	753.6	87.5	969	3	AAA75164
23	753.6	87.5	969	3	AAA75163 CDNA clon
24	753.6	87.5	969	3	AAA75165 CDNA clon
25	753.6	87.5	1140	10	AA660105 Human and
26	753.6	87.5	1140	10	ADH62276 Human PME
27	753.6	87.5	1140	12	ADP39826 Human PME
28	753.6	87.4	759	10	ADP17545 Human and
29	752.8	87.4	759	10	ADH62277 Human PME
30	752.8	87.4	759	12	ADO39827 Human PME
31	752.6	87.4	806	3	ACC49537 Tumour-as
32	752.6	87.4	1061	3	AAA47429 Sequence
33	752.6	87.4	1085	10	ADP37324 Nuclea
34	752.6	87.4	1334	8	ABZ36103 Human sec
35	752.6	87.3	4531	14	AEB22833 Human col
36	742.4	86.2	1066	4	AA159654 Human pol
37	712	82.7	1069	4	AA159654 Human pol
38	612.4	71.1	878	6	ABK12142 Mouse CDN
39	544.4	63.2	1583	6	AB861424
40	462.2	53.7	1713	3	AAA75152
41	460.6	53.5	1713	3	AAA75167
42	460.6	53.5	1713	3	AAA75166 CDNA clon
43	460.6	53.5	1713	3	AAA75168 CDNA clon
44	445.6	51.8	693	6	ABK12143 Human MIV
45	417.4	48.5	812	2	AAZ52964 Human pro

ALIGNMENTS

RESULT 1	
ADN38809	ADN38809 standard; cDNA; 864 BP.
XX	ADN38809;
XX	17-JUN-2004 (first entry)
XX	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:127.
XX	Human; differential expression; cancer; angiogenic disorder;
KW	fibrotic disorder; porosis; ischaemia; heart disease; atherosclerosis;
KW	inflammatory disease; autoimmune disease;
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;
KW	detection; diagnosis; prognosis; drug screening; drug targeting;
KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW	vulnerable; gene therapy; vaccine; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2003042661-A2.
XX	
PD	22-MAY-2003.
XX	
XX	13-NOV-2002; 2002WO-US036810.
XX	
XX	13-NOV-2001; 2001US-0350666P.
XX	21-NOV-2001; 2001US-0332464P.
PR	29-NOV-2001; 2001US-034393P.
PR	03-DEC-2001; 2001US-0335394P.
PR	14-DEC-2001; 2001US-0340376P.
PR	08-JAN-2002; 2002US-0347211P.
PR	10-JAN-2002; 2002US-0347349P.
PR	08-FEB-2002; 2002US-0355250P.
PR	13-FEB-2002; 2002US-0356714P.
PR	20-FEB-2002; 2002US-0359077P.
PR	29-MAR-2002; 2002US-0368809P.
PR	04-APR-2002; 2002US-0370110P.
PR	12-APR-2002; 2002US-0372246P.
PR	05-JUN-2002; 2002US-0386614P.
PR	16-JUL-2002; 2002US-0396839P.
PR	22-JUL-2002; 2002US-0397775P.















RESULT 8  
ADR65875  
ID ADR65875 standard; DNA; 4839 BP.  
XX  
AC ADR65875;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human prostatic carcinoma derived DNA SEQ ID 71 #1.  
XX  
KM human; cytostatic; diagnosis; prostatic cancer;  
XX differential expression analysis; ds.  
OS Homo sapiens.  
XX  
PN WO2004076614-A2.  
XX  
PD 10-SEP-2004.  
XX  
PF 22-FEB-2004; 2004WO-DE000433.  
XX  
PR 27-FEB-2003; 2003DE-01009985.  
XX 14-MAY-2003; 2003DE-01022134.  
PR  
XX  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILAR/) PILARSKY C.  
XX  
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinemann H, Roepecke S;  
PI Xinhong L, Staub E;  
XX  
DR WPI; 2004-653386/63.  
XX  
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX  
PS Claim 1; Page 277; 1607pp; German.  
XX  
XX This invention describes novel cytosstatic polynucleotide and polypeptide  
XX sequences which can be used in a method for diagnosing prostatic cancer  
XX or the risk of developing prostatic cancer. Diagnosis is based on  
XX determining over transcription or over expression of the sequences in  
XX prostatic tissue. Screening for inhibitors of the sequences or detection  
XX substances involves a binding assay, any compounds that bind are  
XX selected, optionally after deconvolution of mixtures. Detection of a  
XX predetermined minimum level of the reporter indicates the presence of  
XX tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
XX short-interfering RNA or ribozymes; an organic molecule of molecular  
XX weight below 5000, preferably 300, that binds to the polypeptide; an  
XX aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
XX polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
XX (monoclonal) antibody directed against Ab or any of the above derivatised  
XX with a reporter group, cell toxin, immunostimulatory molecules and/or  
XX radioisotope. The polynucleotides are identified in human prostatic  
XX cancer by differential expression analysis, using DNA microarrays,  
XX between normal and tumorous tissues, with (over)expression being detected  
XX by quantitative PCR. Analysis of prostatic cancer samples showed that  
XX CD24 was upregulated in many of them. Sections of tissue, isolated from  
XX prostatic cancer patients, or subjects at risk, were incubated  
XX sequentially with anti-human CD4 murine monoclonal antibodies;  
XX biotinylated second antibody; streptavidin-conjugated horseradish  
XX peroxidase and then diamnobenzydine as colour former (brown). The  
XX samples were counterstained with hemalum (blue). Malignant cells stained  
XX strongly but non-malignant cells only weakly. In 15 of 63 samples of  
XX adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
XX lymph node metastases were also stained. ADR65805-ADR65954 represent the  
XX polynucleotide and polypeptide sequences used in the method of the

CC invention.  
XX  
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 861; DB 13; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 3.3e-167;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 1 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCGCGCGCGGACGCCCAATGTC 60  
DB 321 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCGCGCGCGGACGCCCAATGTC 380  
QY 61 TCCTGACAGTGAATGCAATGCAAAAGCTCTTGTTCAGACATGAGATCAAGAGCTGAG 120  
DB 381 TCCTGACAGTGAATGCAAAAGCTCTTGTTCAGACATGAGATCAAGAGCTGAG 440  
QY 121 TTTGTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180  
DB 441 TTTGTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 500  
QY 181 CTGCTGAGCCACTACAGAGCTGTTCACAGGTCCTTCATCAGCCGACACAGCGGGCGG 240  
DB 501 CTGCTGAGCCACTACAGAGCTGTTCACAGGTCCTTCATCAGCCGACACAGCGGGCGG 560  
QY 241 AGGAGAGAAAGATGCCCTGCTCCAGAGAGATGCTGAGCCCTCGGAGAGACAGTGTCA 300  
DB 561 AGGAGAGAAAGATGCCCTGCTCCAGAGAGATGCTGAGCCCTCGGAGAGACAGTGTCA 620  
QY 301 GGCACACGAGATCCACAGAGCCGAGGTCTACGCGCCGCTCGGACACGCGCTGAGCC 360  
DB 621 GGCACACGAGATCCACAGAGCCGAGGTCTACGCGCCGCTCGGACACGCGCTGAGCC 680  
QY 361 GTGCGCGCCCTTGCCCAAGCGGAGGCTTCCACAGCGCTTCCAGCCCACTATCCGACTG 420  
DB 681 GTGCGCGCCCTTGCCCAAGCGGAGGCTTCCACAGCGCTTCCAGCCCACTATCCGACTG 740  
QY 421 CAGCAGAGATGACCTGACACCCACCATCTGCTGTGACAGCGGAGAGAGCCCAACC 480  
DB 741 CAGCAGAGATGACCTGACACCCACCATCTGCTGTGACAGCGGAGAGAGCCCAACC 800  
QY 481 TACAGAGGCGCCCTGACACCCCTTCAGGCTTGCGGAGCCCGAGCAGAGCTGAACTGAA 540  
DB 801 TACAGAGGCGCCCTGACACCCCTTCAGGCTTGCGGAGCCCGAGCAGAGCTGAACTGAA 860  
QY 541 GAGTGTGTGCGGCGCACCCCAAGAACATCTTTCAGACGATGATGATGATGATGATG 600  
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QY 601 AGGCTGGGCGGCGCCGCGCCCGCAGAGTAACTGCGGATCAGCGCCACGTCTACGGC 660  
DB 921 AGGCTGGGCGGCGCCGCGCCCGCAGAGTAACTGCGGATCAGCGCCACGTCTACGGC 980  
QY 661 AGCGCGGGCGGCGATGAGAGGGGCGCGCCCACTTACAGGAGATCATGCGGCACTACCG 720  
DB 981 AGCGCGGGCGGCGATGAGAGGGGCGCGCCCACTTACAGGAGATCATGCGGCACTACCG 1040  
QY 721 GGGTCTCTCTTTCAGACATCAGACAGCACTGCGGCGCTCTTCTGAGAGGGACCGG 780  
DB 1041 GGGTCTCTCTTTCAGACATCAGACAGCACTGCGGCGCTCTTCTGAGAGGGACCGG 1100  
QY 781 CTCACACACACACATGCGCGCCCTTAGAGAGCGAGCATCTGAGAGCAAGAGAT 840  
DB 1101 CTCACACACACACATGCGCGCCCTTAGAGAGCGAGCATCTGAGAGCAAGAGAT 1160  
QY 841 AAACAGAAAGACACCTCTC 861  
DB 1161 AAACAGAAAGACACCTCTC 1181  
XX  
RESULT 9  
ADR66778  
ID ADR66778 standard; DNA; 4839 BP.  
XX







CC The present invention relates to novel nucleic acid sequences that are  
CC expressed by human prostate cancer cells. The nucleic acid sequences or  
CC the encoded proteins are useful as targets for treating, preventing  
CC and/or diagnosing cancers, particularly prostate cancer. The present  
CC sequence is one such nucleic acid of the invention.

XX Sequence 4839 BP, 1103 A, 1313 C, 1290 G, 1133 T, 0 U, 0 Other:

Query Match 100.0%; Score 861; DB 14; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 3.3e-167;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCACCGCTTGTGATGGGGGTCAACAGACCGCCGCCGCCGCCGCCGCCGCCCATGTC 60
DB ATGCACCGCTTGTGATGGGGGTCAACAGACCGCCGCCGCCGCCGCCGCCCATGTC 360
QY 61 TCCTGACGTCGCAACTGCAAGCGCTTTGTTCAGAGATGAGATCAAGAGCTGAG 120
DB TCCTGACGTCGCAACTGCAAGCGCTTTGTTCAGAGATGAGATCAAGAGCTGAG 440
QY 121 TTGTTCAAGATCATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB TTGTTCAAGATCATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
QY 181 CTGCTGAGCCACTCAAGAGCTGTGTCAGCGGTCTTTCATCAGCCGCGCACAGCCAGGGCCG 240
DB CTGCTGAGCCACTCAAGAGCTGTGTCAGCGGTCTTTCATCAGCCGCGCACAGCCAGGGCCG 560
QY 241 AGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB AGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
QY 301 GGCACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB GGCACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
QY 361 GTGCGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB GTGCGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
QY 421 CACGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB CACGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
QY 481 TACGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB TACGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
QY 541 GAGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB GAGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 920
QY 601 AGGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB AGGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 980
QY 661 AGGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB AGGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
QY 721 GAGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB GAGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1100
QY 781 CTGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB CTGACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1160
QY 841 AAACAGAAAGACACCTCTTC 861
DB 1161 AAACAGAAAGACACCTCTTC 1181
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## RESULT 12

ACN40804  
ID ACN40804 standard; cDNA; 4911 BP.

AC ACN40804;

DT 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.

DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;

XX Tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW central nervous system cancer; bladder cancer; pancreatic cancer;

KW cervical cancer; melanoma; leukaemia; hybridisation probe;

KW chromosome identification; chromosome mapping; gene mapping;

XX gene therapy; cytostatic; gene; ss.

OS Homo sapiens.

PN WO2004030615-A2.

XX 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GENTH ) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX New tumor-associated antigenic target polypeptides and nucleic acids,

XX useful in preparing a medicament for treating or detecting a

XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or

XX prostate cancer or tumor.

XX Claim 1; SEQ ID NO 5823; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)

XX polypeptides, and their related nucleic acids. The TAT polypeptides are

XX overexpressed in cancer tissues compared to normal tissues, and may thus

XX serve as effective targets for the diagnosis and treatment of cancer in

XX mammals. The invention also relates to nucleic acid and polypeptide

XX sequences at least 80% identical to the TAT nucleic acids and

XX polypeptides; expression vectors and host cells comprising a TAT nucleic

XX acid, an antibody specific for a TAT polypeptide; a peptide or organic

XX molecule which binds to a TAT polypeptide; fusion proteins comprising a

XX TAT polypeptide; and methods and compositions for the treatment or

XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

XX antibodies, antagonists, binding molecules and compositions are useful

XX for diagnosing or treating a cell proliferative disorder associated with

XX increased TAT expression, particularly cancers such as breast cancer,

XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder

XX cancer, pancreatic cancer, cervical cancer, cancers of the central

XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be

XX used as hybridisation probes, in chromosome and gene mapping, in

XX chromosome identification and in gene therapy. The present sequence

XX represents a TAT nucleic acid of the invention

XX

XX Sequence 4911 BP, 1114 A, 1331 C, 1324 G, 1142 T, 0 U, 0 Other:

Query Match 100.0%; Score 861; DB 13; Length 4911;  
Best Local Similarity 100.0%; Pred. No. 3.3e-167;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCACCGCTTGTGATGGGGGTCAACAGACCGCCGCCGCCGCCGCCGCCCATGTC 60
DB 393 ATGCACCGCTTGTGATGGGGGTCAACAGACCGCCGCCGCCGCCGCCGCCCATGTC 452
QY 61 TCCTGACGTCGCAACTGCAAGCGCTTTGTTCAGAGATGAGATCAAGAGCTGAG 120
```





OY	181	TTGCTGAGCCACTTCAAGCTGTGTGCAGAGGCTCTTCAATCAACCGGCACAGCCAGGGCCGG	240
Db	574	CTGCTGAGCCACTTCAAGCTGTGTGTGCAGAGGCTCTTCAATCAACCGGCACAGCCAGGGCCGG	633
OY	241	AGGAGAGAAAGATGCGCTGTCTCTCAGAAAGATGCTGTGTGACCCTCGAGAGCACAGTGTCA	300
Db	634	AGGAGAGAAAGATGCGCTGTCTCTCAGAAAGATGCTGTGTGACCCTCGAGAGCACAGTGTCA	693
OY	301	GGCAACGGAAATCCAGAGCCGAGGTCTAAGCCCGCCGCTCGGCCCACTGACCCGCTTGACC	360
Db	694	GGCAACGGAAATCCAGAGCCGAGGTCTAAGCCCGCCGCTCGGCCCACTGACCCGCTTGACC	753
OY	361	GTGCGCGCCCTTGGCCAGCGGAGGCGTTCACACGCTTCAGAGCCACTATCCGTAACCTG	420
Db	754	GTGCGCGCCCTTGGCCAGCGGAGGCGTTCACACGCTTCAGAGCCACTATCCGTAACCTG	813
OY	421	CAGCACGAGATGCACTGTGCACCCACATCTCGCTGTCAAGCGGGAGAGACCCGCCACC	480
Db	814	CAGCACGAGATGCACTGTGTGCACCCACATCTCGCTGTCAAGCGGGAGAGACCCGCCACC	873
OY	481	TACCAAGGCCCCCTGCAACCTCCAGCTTGGGAGCCCGAGCAGCAGCTGAACTGAACCGG	540
Db	874	TACCAAGGCCCCCTGCAACCTCCAGCTTGGGAGCCCGAGCAGCAGCTGAACTGAACCGG	933
OY	541	GAGTGTGTGCGCGCACCCCCAAACAAACATCTTTCAGACGTGACCTGAATGATGTGCC	600
Db	934	GAGTGTGTGCGCGCACCCCCAAACAAACATCTTTCAGACGTGACCTGAATGATGTGCC	993
OY	601	AGGCTGTGGGCGGCCCCCTGCCCCCGACAGATTACTGGGCATTCAGCGCCACAGTGTCAACGGC	660
Db	994	AGGCTGTGGGCGGCCCCCTGCCCCCGACAGATTACTGGGCATTCAGCGCCACAGTGTCAACGGC	1053
OY	661	AGCGCGGGCGCATGAGGGGGCGCGCGCCACTTACAGCGAGGTTCATCGGCCACTAACCGG	720
Db	1054	AGCGCGGGCGCATGAGGGGGCGCGCGCCACTTACAGCGAGGTTCATCGGCCACTAACCGG	1113
OY	721	GGGTCTCTCTTCAGACCCAGCAGACGACGTGGGCGCCCTCTCTTGTGAGGGGACCCGG	780
Db	1114	GGGTCTCTCTTCAGACCCAGCAGACGACGTGGGCGCCCTCTCTTGTGAGGGGACCCGG	1173
OY	781	CTTCACACACACACATATCGCGCCCTTAAGAGCCGACGCAATCTGAGGAAAGAGAGGAT	840
Db	1174	CTTCACACACACACATATCGCGCCCTTAAGAGCCGACGCAATCTGAGGAAAGAGAGGAT	1233
OY	841	AAACGAAAGGACACACCTCTC	861
Db	1234	AAACGAAAGGACACCTCTCTC	1254

RESULT 14  
ADC37326  
ID ADC37326 standard; DNA; 1383 BP.

AC ADC37326;

DT 18-DEC-2003 (first entry)

DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.

KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease  
KW cancer; infectious disease; bone disease; AIDS;  
KW neurodegenerative disease; ischaemic disorder; Anti-inflammatory;  
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;  
KW Immunoprotective; Nocturnal; Cardiant; Gene therapy; human; gene, ds  
XX  
XX Homo sapiens.  
OS

PN WO2003048202-A2.

PD 12-JUN-2003.

PF 03-DEC-2002; 2002WO-JP012644.

XX 03-DEC-2001; 2001JP-00368692.  
PR 05-DEC-2001; 2001US-0335829P.  
PR 03-OCT-2002; 2002JP-0029130Z.  
PR 04-OCT-2002; 2002US-0415769P.  
PR

PA (ASAH ) ASahi KASEI KK.  
 PA  
 XX

PI Matsuda A, Muramatsu S;  
 YV

DR WPI; 2003-505282/47.  
DR P-BENB A ANDC37327

XX Nov 27 1964

useful for treating inflammation, autoimmune diseases, cancers, bone diseases AIDS, neurodegenerative diseases or infectious diseases

PT ischemic disorders.  
vvy

PS Claim 4; SEQ ID NO 159; 938bp; English.

CC The present invention relates to novel proteins and their coding  
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF  
CC kappaB). The proteins and their coding sequences are useful for treating  
CC a disease associated with NF-kappaB activation, such as inflammation,  
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,  
CC neurodegenerative diseases, or ischaemic disorders.

**SQ** Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;

Query Match	99.8%	Score 859.4;	DB 10;	Length 1383,
Database	99.8%	Prod No 5	99-167;	

Matches	860;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

1 ATGCACCGCTGATGGGGTCAACAGCACCGCCGCCGCCCGCCGCGGAGCCCAATGTC 60

Dd 321 ATGCACCGCTGATGGGGTCAACAGCACCGCCGCCGCCGCCGCGGCAAGCCAAAGC 380

61 TCCTGCACGTGCAACTGCAACGCTCTTTGTTCAGAGCAATGGAGATCACGGAGCTGGAG 120

Db 381 TCCTGCACGTGCAACTGCMAACGGCTCTTGTGTTCCAGAGCAIIGAGATCACGGAGCTGGAG 440

121 TTTGTCAGATCATCATCGTGGTGAAGAAGGAGGAGCAGGAC

Db 441 TTTGTCAGATCATCATCGTGGTGGAIGAI GGIGIGI GAI CACGTC

181 CTGCTGAGCCACTACAGCTGTCTGCACGGTCCATCAGCCCGCACAGCCAGGCGG 240

Db 501 CTGCTGAGCCACTACAAAGCTGTCTGCAAGGTCCTTCAIACAGCCGGCAACAGCCAGGCGG 56

241 AGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCCTGTGGCCCTCGAGAGCAACAGTGTCA 300

Db 561 AGGAGAGAGATGCCCTGTCTCAGAGGATGCCCTGTGGCCCTCGGAGAGCAAGTGTCA 620

301 GGCAACGGATCCAGAGCCGCAAGTCTACGCCCCGCTTGGCCATCCAGCCGCTGGC 360

Db 621 GGCAACGGATCCAGAGCCCGCAGTCTACGCCCCCGCTCGGCCAACCGACCGCTGGC 680

361 GTGCCGCCCTTGGCCAGCCGGAGCGCTTCCACCGCTTCCAGCCCACTATCCGTAACCTG 420

Db 681 GTGCCGCCCTTCGCCCCAGCGGAGCGCTTCACCGCTTCAGCCACCTAATCCGTAACCTG / 40

421 CAGCAGAGATGACCTGCCACCCACCATCTCGTGT CAGACGGGAGAGCCCCACCC 480

Db 741 CAGCAGAGATCGACCTGCCGCCACCACTCTGGCTGTGAGACGGGAGGACCCCAACC 800

481 TACCAGGGCCCCCTGCACCCCTCCAGCTTCGGALCCCGAGCAGCAGCTGGAACCGAACCG 34

DB 801 TACCAGGGCCCCCTGCACCTTCCAGCTTCGGACCCGAGCAGCAGCTGGATCGATCG 800

541 GAGTCGGTGGCCACCCCAACAGAACATCTTCAGCAGTGAATGATATGTC

[illegible]

QY 601 AGGCTGGGGGCGCCCTGCCCCCAGAGTACTGGGGGATGAGGCCAGTGTACGGC 660  
DB 921 AGGCTGGGGGCGCCCTGCCCCCAGAGTACTGGGGGATGAGGCCAGTGTACGGC 980  
QY 661 AGGCGGCGGCGGATGAGGAGGCGCGCCGACCTTACAGGAGGTATCGGCCATTACCG 720  
DB 961 AGGCGGCGGCGGATGAGGAGGCGCGCCGACCTTACAGGAGGTATCGGCCATTACCG 1040  
QY 721 GGGTCTCTCTTCCAGACCAAGACGATGGGCGCGCTCTTCTGTGGAGGGACCCGG 780  
DB 1041 GGGTCTCTCTTCCAGACCAAGACGATGGGCGCGCTCTTCTGTGGAGGGACCCGG 1100  
QY 781 CTCGACCAACACATGCGCGCCCTTACAGGAGGAGGATCGTGGAGGAGGAGAT 840  
DB 1101 CTCGACCAACACATGCGCGCCCTTACAGGAGGAGGATCGTGGAGGAGGAGAT 1160  
QY 841 AAACAGAAAGACACCCCTCTC 861  
DB 1161 AAACAGAAAGACACCCCTCTC 1181

RESULT 15  
ID AAA75151  
XX AAA75151 strand; cDNA; 969 BP.

AC AAA75151;

DT 15-JAN-2001 (first entry)

XX cDNA encoding a human TANGO 261 polypeptide.

XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;  
XX cellular proliferation; cellular differentiation; cellular adhesion;  
XX von Willebrand factor-associated disorder; cell trafficking; cancer;  
XX hemolytic associated disease; atelectasis; pulmonary congestion;  
XX oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;  
XX intestinal disorder; spleen associated disease; renal disorder;  
XX cardiovascular disorder; ischemic heart disease; hydrocephalus;  
XX brain herniation; iatrogenic disease; inflammation; meningitis;  
XX Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;  
XX multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 6..764  
FT /\*tag= a

FT sig\_peptide 6..89  
FT /\*tag= b

FT mat\_peptide 90..764  
FT /\*tag= c

XX WO20052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005226.

XX 01-MAR-1999; 99US-012458P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX WPI; 2000-579269/54.

XX P-PSDB; AAB18449.

XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,  
XX 266 and 267 useful as modulating agents of cellular processes, e.g. for  
XX treating cancer.

XX Claim 2; Fig 5; 175pp; English.

XX The present sequence encodes a human TANGO 261 polypeptide. The  
CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO  
CC 267. The TANGO polypeptides can be used to modulate cellular  
CC proliferation, modulate cellular differentiation and/or modulate cellular  
CC adhesion. The proteins can be used to treat any von Willebrand factor-  
CC associated disorder, regulate extracellular matrix structuring, cellular  
CC adhesion, and cell trafficking and/or migration, modulate cellular  
CC interactions, modulate cell adhesion in proliferative disorders, such as  
CC cancer, modulate the proliferation, differentiation, and/or function of  
CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,  
CC blood and hematopoietic associated diseases and disorders, atelectasis,  
CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial  
CC asthma and bronchiectasis, intestinal disorders, spleen associated  
CC diseases, modulate renal disorders, treat cardiovascular disorders such  
CC as ischemic heart disease, modulate the proliferation, differentiation,  
CC and/or function of bone and cartilage cells and to treat bone and/or  
CC cartilage associated diseases or disorder. They may also be used to treat  
CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,  
CC brain herniations, iatrogenic disease, inflammation, bacterial and viral  
CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's  
CC disease, multiple sclerosis, brain cancers, hydrocephalus and  
CC encephalitis, and treat hepatic disorders

Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;

Query Match 87.7%; Score 755.2; DB 3; Length 969;

Best Local Similarity 99.6%; Pred. No. 1.4e-145; Mismatches 0; Gaps 0;

Matches 757; Conservative 0; Indels 0; Gaps 0;

QY 102 GGAGATCAAGGAGCTGAGTTTGTTCAGATCATCATCTGTTGATGATGATGAT 161

DB 2 GGAGATGCGGAGCTGAGTTTGTTCAGATCATCATCTGTTGATGATGATGAT 61

QY 162 GGTGTGTGATCACTGCTGCTGACCACTACAGCTGTCTGACGCTCTTATCAG 221

DB 62 GGTGTGTGATCACTGCTGCTGACCACTACAGCTGTCTGACGCTCTTATCAG 121

QY 222 CCGGACAGCGAGGGGCGAGAGAGATGCGCTGCTGAGAGATGCTGTGCGC 281

DB 122 CCGGACAGCGAGGGGCGAGAGAGATGCGCTGCTGAGAGATGCTGTGCGC 181

QY 282 CTGGAGAGACAGTGTCAAGGCAAGGAATCCCAAGCGCAGTCTACGCCCCCTCG 341

DB 182 CTGGAGAGACAGTGTCAAGGCAAGGAATCCCAAGCGCAGTCTACGCCCCCTCG 241

QY 342 GCCACCGACCGCTGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACGCTTCCA 401

DB 242 GCCACCGACCGCTGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACGCTTCCA 301

QY 402 GCCACCTATTCGTATCTGACAGAGATGCACTGCGACCCACATCTGCTGTGAGA 461

DB 302 GCCACCTATTCGTATCTGACAGAGATGCACTGCGACCCACATCTGCTGTGAGA 361

QY 462 CCGGAGAGAGCCCGACCTTACAGAGGCGCTTGCACCTTCACTTGGGACCCGAGCA 521

DB 362 CCGGAGAGAGCCCGACCTTACAGAGGCGCTTGCACCTTCACTTGGGACCCGAGCA 421

QY 522 GCACTGTGAATGAACCGGAGTGGTGGCGGACCCCAAGAAAGAAATCTTGGACAG 581

DB 422 GCACTGTGAATGAACCGGAGTGGTGGCGGACCCCAAGAAAGAAATCTTGGACAG 481

QY 582 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641

DB 482 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541

QY 642 CAGCGCAAGTGTCTACAGGAGCGGCGGAGTGAAGGGGCGCGCCACTTACAGCGCA 701

DB 542 CAGCGCAAGTGTCTACAGGAGCGGCGGAGTGAAGGGGCGCGCCACTTACAGCGCA 601

QY 702 GGTTCATCGGCACTACCGGCGGCTCTCTTCCAGACCAAGAGAGATGGGCGCGCTTC 761

DB 602 GGTTCATCGGCACTACCGGCGGCTCTCTTCCAGACCAAGAGAGATGGGCGCGCTTC 661

Qy	Db	Qy	Db
762	662	822	722
CTGTGTGGAGGGGACCCGGCTCCACACACACATCGCGCCCTTGAAGACGACGCAT	CTGTGTGGAGGGGACCCGGCTCCACACACACATCGCGCCCTTGAAGACGACGCAT	CTGGAGCAAGAGAGATTAACAGAAAGACACCCCTTTC	CTGGAGCAAGAGAGATTAACAGAAAGACACCCCTTTC

Search completed: February 28, 2006, 09:33:18  
Job time : 588.364 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:05:04 ; Search time 3986.56 Seconds  
(without alignments)  
10104.861 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861  
Sequence: 1 atgcacgccttgatggggggt.....aacagaagacacccttc 861

Scoring table: IDENTITY NUC  
Gapop 10'-0', Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hic:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_ges1:  
10: gb\_ges2:  
11: gb\_ges3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	811.8	94.3	1005	AL578575	AL578575 AL578575
C 2	807.6	93.8	1038	AL517150	AL517150 AL517150
3	743.6	86.4	967	BQ641849	BQ641849 AGENCOURT
4	700	81.3	1046	BM922276	BM922276 AGENCOURT
5	693	80.5	901	CR612083	CR612083 full-length
6	687.7	79.9	945	BU539219	BU539219 AGENCOURT
C 7	686.2	79.7	850	AL558881	AL558881
8	667.4	77.5	916	BQ954555	BQ954555 AGENCOURT
C 9	667.7	77.5	867	BX362386	BX362386
10	666.6	77.0	897	AL558882	AL558882
11	662.8	77.4	850	BU602918	BU602918 AGENCOURT
12	648	75.3	780	AY419334	AY419334 Homo sapi
13	637.4	74.0	647	DN992322	DN992322 TC124411
14	607.4	70.5	609	BQ636742	BQ636742 hdl3h06.Y
15	603.6	70.1	1207	AK008976	AK008976 Mus muscu
16	591.4	68.7	601	DN991959	DN991959 TC113206
17	588.8	68.4	605	CV028567	CV028567 7115 Full
18	578.4	67.2	890	BQ690750	BQ690750 AGENCOURT
19	570.4	66.2	973	BU169156	BU169156 AGENCOURT
20	568.8	66.1	572	BX641317	BX641317 DKF2686K
C 21	568.2	66.0	782	BQ015170	BQ015170 UT-H-ED1-
22	550	63.9	551	BM141979	BM141979 if25a11.Y

23	545	63.3	553	8	DN990606	DN990606 TC121025
24	529.8	61.5	894	3	BI851941	BI851941 603379004
C 25	519.4	60.3	729	5	BQ575741	BQ575741 UT-H-EZ1-
C 26	516.8	60.0	730	3	BM677602	BM677602 UT-B-B01-
C 27	515.2	59.8	728	5	BU683523	BU683523 UT-CF-B01
28	504	58.5	780	10	AY419335	AY419335 Pan trogl
29	501.6	58.3	588	3	BM483503	BM483503 536869 MA
30	496.8	57.7	711	7	CJ028468	CJ028468 C028468
31	487.8	56.7	1059	1	AL543170	AL543170 AL543170
32	487.6	56.6	624	10	CG784226	CG784226 FHRC-CGT-
33	475.2	55.2	624	10	AY419336	AY419336 Mus muscu
34	468	54.4	857	2	BG323347	BG323347 60242173
C 35	465.8	54.1	744	5	BU414421	BU414421 603670223
C 36	461	53.5	763	3	BI764175	BI764175 603276395
C 37	445.6	51.8	692	1	AT761441	AT761441 W965F07.X
38	445.4	51.7	655	5	BQ691705	BQ691705 AGENCOURT
39	445.4	51.7	1280	5	BQ691500	BQ691500 AGENCOURT
40	443.6	51.5	651	6	CB554226	CB554226 MMSF0052
41	440	51.1	899	5	BU196912	BU196912 AGENCOURT
42	432.8	50.3	964	5	BU859860	BU859860 AGENCOURT
43	430	49.9	841	2	BI156703	BI156703 602922119
44	429.6	49.9	646	5	BU859841	BU859841 AGENCOURT
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#### ALIGNMENTS

RESULT 1  
LOCUS AL578575/c 1005 bp mRNA linear EST 07-APR-2004  
DEFINITION AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
CDNA clone CS0DX001YC24 3-PRIME, mRNA sequence.  
ACCESSION AL578575  
VERSION AL578575.3 GI:46257448  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 1005)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 16, 2001 this sequence version replaced gi:31316780.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9945.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna/s=CS0DX001B12NP1&c=9945.r.  
Location/Qualifiers  
1..1005  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

#### FEATURES

source

ORIGIN





[illegible]

RESULT 3					
B0641849	B0641849	967 bp	mRNA	linear	EST 15-JUL-2007
LOCUS					
DEFINITION	AGENCOCURT 8287174 NIH_MGC_43	Homo sapiens	CDNA clone IMAGE:6292265		
	5', mRNA sequence.				

ACCESSION	BO641849	GI:21766021
VERSION	BO641849.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 967)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC).  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC  
CNA Library Preparation: Rubin Laboratory  
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: L10C2493 row: g column: 18  
High quality sequence stop: 571.  
Location/Qualifiers  
1..967

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)

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ORIGIN	Note: this is a NIH_MGC Library.   "
Query Match	86.4%; Score 743.6; DB 5; Length 967;
Best Local Similarity	99.5%; Pred. No. 1.7e-15;
Matches 746; Conservative	0; Mismatches 4; Indels 0; Gaps 0

[illegible]

RESULT 4					
LOCUS	BM922276				
DEFINITION	BM922276	1046 bp	mRNA	linear	EST 12-MAR-2000
ACCESSION	AGENCOURT 6707077	NIH_MGC_115	Homo sapiens	cDNA clone	IMAGE:5754433
VERSION	BM922276				
KEYWORDS	BM922276.1	GI:19372655			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homnidae; Homo.				



OY	229	AGCCAGGGGGCGAGAGAGAAAGATGGCCCTGTCTTCAGAAAGATGCTGTGGCCCTCGGAG	288
Db	61	AGCCAGGGGGCGAGAGAGAAAGATGCCCTGTCTTCAGAAAGATGCTGTGGCCCTCGGAG	120
OY	289	AGCAGATGTCAAGGCACGGAATCCGAGAGCCGCGAGGTCTACGCTCCGCTCGGCCAC	348
Db	121	AGCAGATGTCAAGGCACGGAATCCGAGAGCCGCGAGGTCTACGCTCCGCTCGGCCAC	180
OY	349	GACCGCCCTGGGCGGTGCGGCCCTTTCGCGCCAGGGGAGGCGCTTCACCGCTTCAGGCCAC	408
Db	181	GACCGCCCTGGGCGGTGCGGCCCTTTCGCGCCAGGGGAGGCGCTTCACCGCTTCAGGCCAC	240
OY	409	TATCCGTACTCTGCAGCAGAGATGCACCTGCGACACCAATCTCGCTGTCAAGCGGGAG	468
Db	241	TATCCGTACTCTGCAGCAGAGATGCACCTGCGACACCAATCTCGCTGTCAAGCGGGAG	300
OY	469	GAGCCCCACCTTACAGAGGCGCCCTTGACCTTCAGCTTCGGAACCCGAGACGACGTG	528
Db	301	GAGCCCCACCTTACAGAGGCGCCCTTGACCTTCAGCTTCGGAACCCGAGACGACGTG	360
OY	529	GAACTGAACCCGGGAGTCCGTGCGGCGCACCCGCCAACAAGAACATCTTGACAGTGA	588
Db	361	GAACTGAACCCGGGAGTCCGTGCGGCGCACCCGCCAACAAGAACATCTTGACAGTGA	420
OY	589	ATGATTAATGCGCAGGCTGGGCGGCCCTTGCCGCCCCAGCAGTAACTCGGACATCAGCGCC	648
Db	421	ATGATTAATGCGCAGGCTGGGCGGCCCTTGCCGCCCCAGCAGTAACTCGGACATCAGCGCC	480
OY	649	ACGTGCTACGCGCAGCGCGGGCGCATGTGAAGGGGCGCGGCCCACTTACAGCGAGGTCA	708
Db	481	ACGTGCTACGCGCAGCGCGGGCGCATGTGAAGGGGCGCGGCCCACTTACAGCGAGGTCA	540
OY	709	GGCCCACTACCCGGGGGTCTCTTCCAGCAACAAGAGAGCAGTGGGCGCGCTCTTGTG	768
Db	541	GGCCCACTACCCGGGGGTCTCTTCCAGCAACAAGAGAGCAGTGGGCGCGCTCTTGTG	600
OY	769	GAGGGGACCCGGCTTCAACCAACACATCGCGCTTACAGAGCGCAGCCATCTTGAGC	828
Db	601	GAGGGGACCCGGCTTCAACCAACACATCGCGCTTACAGAGCGCAGCCATCTTGAGC	660
OY	829	AAAGGAAGATTAACAGAAAGACACCTCTC	861
Db	661	AAAGGAAGATTAACAGAAAGACACCTCTCTC	693

RESULT 6	BUS39219	945 bp	mRNA	linear	EST 13-SEP-2002
LOCUS	BUS39219				
DEFINITION	BUS39219	AGENCOURT 10215265 NIH MGC 107 Homo sapiens CDNA clone			
ACCESSION	BUS39219	IMAGE:6565922.5', mRNA sequence.			
VERSION	BUS39219.1	GI:22849660			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 945)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D.				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 945)	NIH-MGC	<a href="http://mgc.nhl.nih.gov/">http://mgc.nhl.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)		
	Contact: Robert Strausberg, Ph. D.			
	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: Rubin Laboratory			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:			
	<a href="http://image.lnll.gov">http://image.lnll.gov</a>			
	Plate: LHC2757	row: P	column: 18	
	High quality sequence stop: 663.			

**FEATURES**  
**Source**

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FEATURES
SOURCE
location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_type="IMAG:6569922"
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/clone_1lb="NIH_MGC.107"
/notes="Organ: breast; Vector: pORF7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT printing.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). Library constructed by
ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH_MGC Library."

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## ORIGIN

Query Match	79.9%	Score 687.8	DB 5	Length 945
Best Local Similarity	96.6%	Pred. No. 4.1e-142		
Matches 734	Conservative	0	Mismatches 23	Indels 3
			Gaps	3

[illegible]

Db 785 CTAAGAGCGGCGCCATCTGTGAGCAAGAGAGATTA 824

RESULT 7  
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LOCUS AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
DEFINITION Homo sapiens cDNA clone CS0D0157P12 3-PRIME, mRNA sequence.  
ACCESSION AL558881 GI:46184268  
VERSION AL558881.3  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 850)  
L1.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31283014.  
COMMENT  
REFERENCE  
AUTHORS Contact: Genoscope  
TITLE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
JOURNAL 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by life technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9945.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdnas=CS0D015D06NP1c-9945.r.  
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/clone="CS0D0157P12"  
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/cell\_line="JURKAT"  
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10-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 79.7%; Score 686.2; DB 1; Length 850;  
Best Local Similarity 99.3%; Pred. No. 9,3e-142;  
Matches 688; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 850 GTGATCAGTCTGCTGAGCCATCAAGCTGTGTGACGGTCTTATCATGCGCGAAC 791  
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Qy 229 AGCCAGGGGCGAGAGAGAAAGATCCCTGTCTTCAAGAGATGCTGTGGCCTCGAG 288  
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Db 790 AGCCAGGGGCGAGAGAGAAAGATCCCTGTCTTCAAGAGATGCTGTGGCCTCGAG 731  
|||||  
Qy 289 AGCACAAGTGTGAGGAAGGAATCCAGAGCGGAGGTACGCCCCCGCTCGGCCACC 348  
|||||  
Db 730 AGCACAAGTGTGAGGAAGGAATCCAGAGCGGAGGTACGCCCCCGCTCGGCCACC 671  
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Qy 349 GACGCGCTGCGCGCTGCGCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 408  
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Db 670 GACGCGCTGCGCGCTGCGCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 611  
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Qy 409 TATCCGTAACCTGCAAGAGATGCACTGCGCACCCACCACTCTGCTGTGACGCGGAG 468  
|||||  
Db 610 TATCCGTAACCTGCAAGAGATGCACTGCGCGCCACCTTCTGCTTCAAGAGCGGAG 551  
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Qy 469 GAGCCCCCACCCTTACAGAGGCGCCCTGACCCCTCAGCTTGAGGAGCCCGAGCAGACTG 528  
|||||  
Db 550 GAGCCCCCACCCTTACAGAGGCGCCCTGACCCCTCAGCTTGAGGAGCCCGAGCAGACTG 491  
|||||  
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Qy 829 AAAGAGAAGATTAACAGAAAGACACCTCTC 861  
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Db 190 AAAGAGAAGATTAACAGAAAGACACCTCTC 158  
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RESULT 8  
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LOCUS B0954555  
DEFINITION AGNCOURT\_8825282 Lupski\_sciatic\_nerve Homo sapiens cDNA clone  
IMAGE:6204609 5', mRNA sequence.  
ACCESSION B0954555  
VERSION B0954555.1 GI:22370033  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 916)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabds-remail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
http://image.llnl.gov  
Plate: LMNL3626 row: c column: 10  
High quality sequence stop: 669.  
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
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Directionally cloned using the following adaptors:  
5'-TCGACCAAGCGTCG-3' and  
5'-GACTAGTTCTGATCGGAGGCGGCCCTT(15)-3'. Size selected >



LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AL558882	AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.	AL558882	AL558882	GI:46184269	EST.	Homo sapiens (human)	1 (bases 1 to 897)	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	On Feb 15, 2001 this sequence version replaced gi:31283015.
Db	630	TAACCTGGGGCATACAGCGCAGCTGTCTAGGCGAGCGCGGGGCGCANTGAGAGGGGCGCGCC	683								
Db	388	TTAACTCGGAGCATACAGCGCAGCTGTCTAGGCGAGCGCGGGGCGCANTGAGAGGGGCGCGCC	329								
Qy	690	CACCTACAGCAGAGGTTCATCGGCGCACTTACCCGGGGGTCTCTCTTCCAGACCCAGCAGAGCAG	749								
Db	328	CACCTACAGCAGAGGTTCATCGGCGCACTTACCCGGGGGTCTCTCTTCCAGACCCAGCAGAGCAG	269								
Qy	750	TGGGCGCGCTCTCTTCTGAGAGGAGACCCCGGCTCCACCAACACACATCGCGCCCTTAGA	809								
Db	268	TGGGCGCGCTCTCTTCTGAGAGGAGACCCCGGCTCCACCAACACACATCGCGCCCTTAGA	209								
Qy	810	GAGCGCAGCCATCTGGAGCAAGAGAGATTAACAGAAAGGACACCCCTTC	861								
Db	208	GAGCGCAGCCATCTGGAGCAAGAGAGATTAACAGAAAGGACACCCCTTC	157								
ORIGIN											
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Best Local Similarity	99.3%	Pred. No. 2.1e-137									
Matches	688	Conservative	2	Mismatches	1	Indels	2	Gaps	2		
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Db	1	GTGATCAGCTGCGCTGTGAGCCACTATCAAGCTGTCTGCAACCGTCTCTTATCATGCGCGGAC	60								
Qy	229	AGCAGGAGGCGGAGAGAGATGCGCTCTCTAGGAAGATGCTGAGGCGCTCGAG	288								

Db	61	AGCCAGGGGGGAGAGAGAAAGATGCCCTTGTCTTCAGAAAGATGCTGTGTGGCCCTCGGAG	120		
QY	289	AGCAAGTGTCTAGGCAACGGAATCCCAAGAGCCGCAAGTCTAAGCCCGGCTCTGGCCAC	348		
Db	121	AGCAGAGTGTCAAGGCAACGGAATCCCAAGAGCCGCA- GTCTTAAGCCCGGCTCTGGCCAC	179		
QY	349	GACCGGCTGTGGCCGTGGCCGCTTGGCCAGGGAGGGAGCTTCACCGCTTCACGCCAC	408		
Db	180	GACCGGCTGTGGCCGTGGCCGCTTGGCCAGGGAGGGAGCTTCACCGCTTTCACGCCAC	239		
QY	409	TATCCGTACTGTGACAGACAGAGATGACCTGTGCACCCACATCTGTGCTGTGACGGGAG	468		
Db	240	TATCCGTACTGTGACAGACAGAGATGACCTGTGCACCCACATCTGTGCTGTGACGGGAG	299		
QY	469	GAGCCCCCACTTACCAAGGAGCCCTTGCACCTTCAAGCTTGGGAGCCCGAGACAGACTG	528		
Db	300	GAGCCCCCACTTACCAAGGAGCCCTTGCACCTTCAAGCTTGGGAGCCCGAGACAGACTG	359		
QY	529	GACTGAAACGGGAGGTGGGTGGGAGACCCCAACGAACATCTTTCAGACGTGACCTG	588		
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QY	589	ATGATAGTGTGCAGAGCTGTGGGCGGCCCTTGCACCCCGCCAGCACTGCTGGGATCAGGCG	648		
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QY	649	ACGTGTCTACGGCAGCGGCGGGCGCATGTGAGGGGCGCGGCCACCTTACAGCGAGGTATC	708		
Db	480	ACGTGTCTACGGCAGCGGCGGGCGCATGTGAGGGGCGCGGCCACCTTACAGCGAGGTATC	539		
QY	709	GGCCACTACCGGGGGTCTCTCTTCAGACACAGACAGACAGTGGGCGGCCCTCTGTGCTG	768		
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QY	769	GAGGGGAGCCCGGCTTCACACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGAGC	828		
Db	600	GAGGGGAGCCCGGCTTCACACACACACACATCGCGCCCTTAGAGAGAGCGCA- SCATCTGAGC	658		
QY	829	AAAGGAAAGATTAAACGAAAGGACACCTCTTC	861		
Db	659	AAAGGAAAGATTAAACGAAAGGACACCTCTTC	691		
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LOCUS	BU602918	850 bp	mRNA linear EST 20-SEP-2002		
DEFINITION	AGENCOURT 10016502 NIH MGC 142 Homo sapiens cDNA clone				
ACCESSION	BU602918	IMAGE:6497853 5', mRNA sequence.			
VERSION	BU602918.1	GI:23254677			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo				
AUTHORS	1 (bases 1 to 850)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strusberg, Ph.D.				
	Email: cgsab@remail.nih.gov				
	Tissue Procurement: NCI				
	cDNA Library Preparation: Michael Brownstein Laboratory				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLN at:				
	http://image.lnl.gov				
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FEATURES	location/Qualifiers				
Source	1..850				







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Db		386	AGCCCCCACCTTAC	CAGGGGCCCTTGCACTCTCAGCTTTGCGGACCCCGAGCAGCAGCTGG	445
Oy		530	AACCTGAACCGGGAA	AGTCGGTGGCGGCAGCCCCAAAAGAACAACATCTTTGACAGTGA	589
Db		446	AACCTGAACCGGGAA	AGTCGGTGGCGGCAGCCCCAAAAGAACAACATCTTTGACAGTGA	505
Oy		590	TGGAATAGTGCAG	GAGCTGGGCGGCCCTGCCCCCGAGCAGTAACTCGGGCAATCAGCGCCA	649
Db		506	TGGAATAGTGCAG	GAGCTGGGCGGCCCTGCCCCCGAGCAGTAACTCGGGCAATCAGCGCCA	565
Oy		650	CGTGTCTTACGCA	GACCGCGGGCGCATATGAGAGGGCGCGGCCCATCTTAACGCGA	709
Db		566	CGTGTCTTACGCA	GACCGCGGGCGCATATGAGAGGGCGCGGCCCATCTTAACGCGA	625
Oy		710	GCAACTACCCCGGG	GGTCTCTTCCAGCACAAGCAGAGAGTAGGGGCGCGCTCTCTTGG	769
Db		626	GCAACTACCCCGGG	GGTCTCTTCCAGCACAAGCAGAGAGTAGGGGCGCGCTCTCTTGG	685
Oy		770	AGGGGACCCGGCT	CCACCAACACATCGCGCCCCTTGAAGGCGCAGCACCATTGGAACA	829
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DEFINITION		DN992322	647 bp	mRNA	linear EST 17-MAY-2005
KEYWORDS			TC124411 Human adult whole brain, large insert, PCMV expression library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEMPR1), transcript variant 4, mRNA sequence.		
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VERSION		DN992322.1	GI:66252153		
SOURCE			EST.		
ORGANISM		Homo sapiens (human)			
REFERENCE			Homo sapiens (human)		
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		
JOURNAL			1 (bases 1 to 647)		
COMMENT			Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W. High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts Unpublished (2005) Contact: Kovacs, KP High Throughput cDNA Cloning Origene Technologies, Inc. ( www.origene.com ) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: cDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: PCMV6 5prime forward vector primer. Origene Technologies Inc. Location/Qualifiers 1..647 /organism="Homo sapiens"		
FEATURES					
SOURCE					

[illegible]

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 609)  
Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human retina for the NEIbank  
Project: Retbindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
Mol. Vis. 8 (4), 196-204 (2002)  
12107411

JOURNAL  
PUBMED  
COMMENT  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 13 row: h column: 06  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
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/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the Superscript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTTCTAGATCGGAGCGCGCCCT(15-3')]. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN  
Query Match 70.5%; Score 607.4; DB 5; Length 609;  
Best Local Similarity 99.8%; Pred. No. 2.9e-124;  
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 CAGCCGGCAGACGCGGCGGAGAGAGAAATGCGCTGCTCAGAGAGATCGCTG 60  
279 GCCCTCGAGAGACAGTGTCAAGCAAGCAATCCAGAGCGCAGAGTCTACCGCCGC 338  
61 GCCCTCGAGAGACAGTGTCAAGCAAGCAATCCAGAGCGCAGAGTCTACCGCCGC 120  
339 TCGGCCACCGACCGCTGCGCGCTGCGCCCTTGCAGCGGAGAGCGCTTCCACGCGCT 398  
121 TCGGCCACCGACCGCTGCGCGCTGCGCCCTTGCAGCGGAGAGCGCTTCCACGCGCT 180  
399 CAGGCCCACTATTCGTAAGTGAAGACAGAGATCGACCTGCCACCACTTCGCTGC 458  
181 CAGGCCCACTATTCGTAAGTGAAGACAGAGATCGACCTGCCACCACTTCGCTGC 240  
459 AGACGGGAGAGAGAGCCCACTTACAGAGGCGCCCTGACCCCTCAGCTTCGGAGACCCGA 518  
241 AGACGGGAGAGAGAGCCCACTTACAGAGGCGCCCTGACCCCTCAGCTTCGGAGACCCGA 300  
519 GCAGCAGCTGGAACCTGAACCGGAGATCGGTGCGCGACCCCCAAACAGAACATCTTCCA 578

Db 301 GCAGCAGCTGGAATGGAACCGGAGATCGGTGCGCGACCCCAACAGAACATCTTCCA 360  
Qy 579 CAGTGACCTGATGATATGATGTCGACAGGCTGGGCGGCCCTTGGCCCCCAGACATTACTGGG 638  
Db 361 CAGTGACCTGATGATATGATGTCGACAGGCTGGGCGGCCCTTGGCCCCCAGACATTACTGGG 420  
Qy 639 CATAGCGCCACAGTGTACAGGACAGCGGCGGCGATGAGAGGAGCGCGCCACCTACAG 698  
Db 421 CATAGCGCCACAGTGTACAGGACAGCGGCGGCGATGAGAGGAGCGCGCCACCTACAG 480  
Qy 699 CGAGGTCAATCGGCGCACTACCGGCGGCTCTCTTCACAGCAGACAGAGAGAGTGGCGGCC 758  
Db 481 CGAGGTCAATCGGCGCACTACCGGCGGCTCTCTTCACAGCAGACAGAGAGAGTGGCGGCC 540  
Qy 759 CTCTTGCTGAGAGGAGACCGCGCTTCACACACACATCGCGCCCTTAGAGAGCGGACG 818  
Db 541 CTCTTGCTGAGAGGAGACCGCGCTTCACACACACATCGCGCCCTTAGAGAGCGGACG 600  
Qy 819 CATCTGGAG 827  
Db 601 CATCTGGAG 609

RESULT 15  
AK008976  
LOCUS  
DEFINITION  
AK008976 1207 bp mRNA linear HTC 03-APR-2004  
Mus musculus adult male stomach cDNA, RIKEN full-length enriched  
library, clone:2210418102 product:Nedd4 WW binding protein 4, full  
insert sequence.  
AK008976 GI:12843488  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
10349636  
2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraktion of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159  
3  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Kono,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Iehi,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
11076861  
4  
THE RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)







MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/091,952A  
FILING DATE: 19-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,278  
FILING DATE: 28-Oct-1996  
APPLICATION NUMBER: PCT/US97/19381  
FILING DATE: 28-Oct-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 015280-297100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1...921  
OTHER INFORMATION: Clone 22 coding region  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-091-952A-7

Query Match 40.9%; Score 352.2; DB 3; Length 921;  
Best Local Similarity 73.1%; Pred. No. 6.2e-69;  
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

94 CAGAGCATGAGATCAAGAGCTGAGAGTTGTTTCAGATCATCATCATCGTGTGATG 153  
166 CCGGGCATCTTCACTGGAGCTGGAGTTGCCCAATCATCATCATCGTGTGATG 225  
154 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 213  
226 ACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285  
214 TTCAATCAGCCGCGACAGCCGAGGCGGAGAGAGAGATGCTGTCTTCAAGAGATG 273  
286 TTCAATCAACCGCCGAGACGAGAGCGGAGAGCGGCTGCGCAGAGAGGATG 345  
274 CTGTGAGCCCTCGAGAGACAGATGTCAGGCAACGGAATCCAGAGCCGAGTTCAGCC 333  
346 CTGTGAGCCCTTCAAGAGAGCGGCGACCGCGGCTGGG-----CGCTCGAGATCATCAT 399  
334 CCGCTCTGCGCCACGACCGGCTGGCGGCTGCGGCTTGGCCAGCGGAGCGCTTCAC 393  
400 GCCCGGCGGTTCAGAGGACAGGTTCAAGCGCGCTTCAATCCAGAGGATCGCTTCAGC 459  
394 CGCTTCAAGCCCATCTTATCCGTACCTGAGAGAGATGACATGACCTGCAACCATTTGG 453  
460 CGCTTCAAGCCCATCTTATCCGTACCTGAGAGAGATGATCTTCTCCACCATTTCC 519  
454 CTGTCAAGCGGAGAGAGCGCCGACCCCTACAGAGGCGCTTGCAGACTTCGAGAC 513  
520 CTGTCCAGCGGTGAAGACCACTTCTTACAGAGGCGCTTGCAGACTTCGAGAC 579  
514 CCGGAGAGAGAGCTGGAATGGAACCGGAGTGGTGGCGGACGCCCAACAGAACTATC 573  
580 CTTGAAGAGAGAGATGGAATCAACGAGAGTCCGTGAGGCGCCCAACCAAGCAATATA 639  
574 TTGACAGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 630

Db 640 TTTCAGATGATTTAATAGATGCTATGATATAGCGGGGATTCATGATCCCAACCAAGCAGC 699  
Qy 631 AACTGGGATATAGCGCCACAGTCTTACAGGAGCGGCGGATGAGAGGCGCGCGCC 690  
Db 700 AACTGGGATATAGCGCCACAGTCTTACAGGAGCGGCGGATGAGAGGCGCGCGCC 759  
Qy 691 AACTGAGGAGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 749  
Db 760 AACTGAGGAGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 818

RESULT 4  
US-09-091-952A-6  
Sequence 6, Application US/09091952A  
Patent No. 6458532  
GENERAL INFORMATION:  
APPLICANT: Deterra-Wadleigh, Sevilla D.  
Gershon, Elliot S.  
Badner, Judith A.  
Goldin, Lynn R.  
Berrettini, Wade H.  
Yoshikawa, Takeo  
Sanders, Alan R.  
Esterling, Lisa E.  
TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/091,952A  
FILING DATE: 19-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,278  
FILING DATE: 28-Oct-1996  
APPLICATION NUMBER: PCT/US97/19381  
FILING DATE: 28-Oct-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 015280-297100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8065 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: -  
LOCATION: 1...8065  
OTHER INFORMATION: Clone 22  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 116...1036  
OTHER INFORMATION: Clone 22 coding region  
FEATURE:  
NAME/KEY: misc\_feature

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; LOCATION: 452...505
; OTHER INFORMATION: alternatively spliced portion
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5595...5685
; OTHER INFORMATION: amplified region for genotyping
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6

Query Match          40.9%; Score 352.2; DB 3; Length 8065;
Best Local Similarity 73.1%; Pred. No. 1e-68;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 94 CAGAGCATGAGATCAACGAGCTGAGAGTTGTTTCATCATATCATCTGCTGATG 153
DB 281 CCGGCGATCTTCACTCGAGAGCTGAGATTGCGCCCAATCATATCATCTGCTGATG 340
QY 154 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 213
DB 341 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400
QY 214 TTTCATCAGCCGAGCAGACCGAGGCGCGAGAGAGAGATGCCCTGCTCAGAGAGATGC 273
DB 401 TTTCATCAGCCGAGCAGACCGAGGCGCGAGAGAGAGATGCCCTGCTCAGAGAGATGC 460
QY 274 CTGTGGCCCTCGAGAGAGCAGCTGTGTAGGCAACGAAATCCAGAGCCGAGGCTTAACGCC 333
DB 461 CTGTGGCCCTCGAGAGAGCAGCTGTGTAGGCAACGAAATCCAGAGCCGAGGCTTAACGCC 514
QY 334 CCGGCTCGGCGCCAGCAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCGGAGGAGGCTTCCAC 393
DB 515 GCGGCGGCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 574
QY 394 CGCTTCAGCCGAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 453
DB 575 CGCTTCAGCCGAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 634
QY 454 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 513
DB 635 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 694
QY 514 CCGGAGCAGAGCTGAGATGAAACCGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 573
DB 695 CCGGAGCAGAGCTGAGATGAAACCGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 754
QY 574 TTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 630
DB 755 TTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 814
QY 631 AACTCGGAGCATCAGCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 690
DB 815 AACTCGGAGCATCAGCTGAGAGCAGCTGATGATGATGATGATGATGATGATGATGATG 874
QY 691 AACTCAGAGGAGTGTATGAGGAGCTGATGAGGAGTGTATGAGGAGTGTATGAGGAG 749
DB 875 AACTCAGAGGAGTGTATGAGGAGCTGATGAGGAGTGTATGAGGAGTGTATGAGGAG 933

RESULT 5
US-09-311-021-65
; Sequence 65, Application US/09311021
;
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fehnel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 65
; LENGTH: 937
; TYPE: DNA
; ORGANISM: Homo sapiens
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; US-09-311-021-65

Query Match          40.8%; Score 351.6; DB 3; Length 937;
Best Local Similarity 73.0%; Pred. No. 8.5e-69;
Matches 482; Conservative 0; Mismatches 169; Indels 9; Gaps 2;

QY 93 CCAGAGCATGAGATCAACGAGCTGAGAGTTGTTTCATCATATCATCTGCTGATG 152
DB 134 CCGTCTTAAAGAGAGGAGCTGAGAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 193
QY 153 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 212
DB 194 CACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 253
QY 213 CTTCATCAGCCGAGCAGACCGAGGCGCGAGAGAGAGATGCCCTGCTCAGAGAGATG 272
DB 254 CTTCATCAGCCGAGCAGACCGAGGCGCGAGAGAGAGATGCCCTGCTCAGAGAGATG 313
QY 273 CCGTGGCCCTCGAGAGAGCAGATGTAGGCAACGAAATCCAGAGCCGAGGCTTAACGCC 332
DB 314 CCGTGGCCCTCGAGAGAGCAGATGTAGGCAACGAAATCCAGAGCCGAGGCTTAACGCC 367
QY 333 CCGGCTCGGCGCCAGCAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCGGAGGAGGCTTCCA 392
DB 368 TGCCCCGCGGTCAGAGGAGCAGAGTTCAACGCGCTGCTTCATCAGAGAGGATGCTTCAG 427
QY 393 CCGCTTCAGGCGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 452
DB 428 CCGCTTCAGGCGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 487
QY 453 GCTGTGAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 512
DB 488 CCGTGTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
QY 513 CCGGAGCAGAGCTGAGATGAAACCGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 572
DB 548 CCGTGTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 607
QY 573 CTTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 629
DB 608 ATTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
QY 630 TAACTCGGAGCATCAGCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 689
DB 668 CAACTCGGAGCATCAGCTGAGAGCAGCTGATGATGATGATGATGATGATGATGATGATG 727
QY 690 CACTCAGAGGAGTGTATGAGGAGCTGATGAGGAGTGTATGAGGAGTGTATGAGGAG 749
DB 728 CACTCAGAGGAGTGTATGAGGAGCTGATGAGGAGTGTATGAGGAGTGTATGAGGAG 787

RESULT 6
US-09-091-952A-8
; Sequence 8, Application US/09091952A
; Patent No. 6458532
;
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; APPLICANT: Gershon, Elliott S.
; APPLICANT: Badner, Judith A.
; APPLICANT: Goldin, Lynn R.
; APPLICANT: Berrettini, Wade H.
; APPLICANT: Yoshikawa, Takeo
; APPLICANT: Sanders, Alan R.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
```



ADDRESSER: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSO for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/091.952A  
 FILING DATE: 19-Apr-1999  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/029,278  
 FILING DATE: 28-OCT-1996  
 APPLICATION NUMBER: PCT/US97/19381  
 FILING DATE: 28-OCT-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, Timothy L.  
 REGISTRATION NUMBER: 35,367  
 REFERENCE/DOCKET NUMBER: 015280-297100US

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 867 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..867  
 OTHER INFORMATION: Clone 22 isoform 2 alternatively  
 spliced coding region

SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 US-09-091-952A-8

Query Match 33.0%; Score 284.2; DB 3; Length 867;  
 Best Local Similarity 68.7%; Pred. No. 7.5e-54;  
 Matches 455; Conservative 0; Mismatches 143; Indels 63; Gaps 2;

94 CAGAGCATGAGATCACGAGCTGAGATTGTTTCATCATCATCTGCTGCTGATG 153  
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 166 CCGGGCATCTTCAACTCGAGCTGAGTTGCCCAATCATCATCTGCTGCTGATG 225  
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 154 ATGTGATGTGTGTGTGATCATGCTGCTGCTGACCACTACAAGCTGTGACGCTGC 213  
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 226 ACGGTATGTGTGTGTGATCTGCTGCTGACCACTACAAGCTGTGACGCTGC 285  
 |||||  
 214 TTGATCAGCCGCGACAGCCAGGGCGGAGAGAGAGATGCCCTGTCTCAGAGATGC 273  
 |||||  
 286 TTGATCAACGCGCCGGAACAGAGCGGAGGCGGAGACGCGGCT----- 329  
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 274 CTGTGCGCTTGGAGAGCAAGTGTCAAGCAAGCAATCCAGAGCCGCGAGTTTACGC 333  
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 330 -----GCCGAGATCATGAT 345  
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 334 CCGCTGGGGCCACCGACCGGCTGGCCGCTTCCGCCAGCGGAGCGCTTCAC 393  
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 346 GCCCGGGGTTCAGGGAGAGTTTACAGCGCGCTTTCATCCAGAGGATCGTTACGC 405  
 |||||  
 394 CGCTTCAAGCCCACTATCCCTACCTGACAGACAGATGACCTGCCACCCCATCTCG 453  
 |||||  
 406 CGCTTCAAGCCCACTATCCCTACCTGACAGACAGATGATTTCTTCTCCCATCTCC 465  
 |||||  
 454 CTGTCAAGCGGGAGAGCCCGCACTTACAGAGGCGCTTCCAGCTTCCGCGGAC 513  
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DB 466 CTGTCCAGCGGTGAAGAGACACTCTTACAGAGGGCCCTTGACCTTCGAGCTCCGGGAC 525  
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 QY 514 CCGGAGCAGCAGCTGGAAGTGAACCGGAGAGTGTGCGCGACCCCAAGAGAACCC 573  
 |||||  
 DB 526 CCTGAACAGCAGATGGAATCAACCGAGAGTCCGAGAGGCCCAACCCAGACATTA 585  
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 QY 574 TTGACAGTGAACCTGATGGAATGATGCGCAGG---CTGGGCGGCCCTGCCCCCAGCACT 630  
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 DB 586 TTGACAGTGAATTTAATGACATTTCTATGTATAGCGGGGGTTCATGCCACCGACAC 645  
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 QY 631 AACTGGGATCAGCGCCACGCTGCTACGCGAGCGCGCGCGCATGAGGGGCGCGCC 690  
 |||||  
 DB 646 AACTGGGATCAGTGAAGACACCTGACAGATTAAGGAGAGGAGGCGCACCCGCC 705  
 |||||  
 QY 691 ACTTACAGCGAGTCAATCGGCCACTACCCGGGCTCTCTTCCAGACAGAGAGCAG 749  
 |||||  
 DB 706 ACATACAGCGAGTATGAGGCGCCACACCGAGCGCTCTTCTTCATCAGAGCGAG 764  
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RESULT 7  
 US-09-621-976-2162  
 ; Sequence 2162, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jober, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621.976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 2162  
 ; LENGTH: 391  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 17..223  
 US-09-621-976-2162

Query Match 10.5%; Score 90.4; DB 3; Length 391;  
 Best Local Similarity 75.7%; Pred. No. 6.3e-11;  
 Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

607 GGGCGCCCTGCCCCCAGAGTAATCTGGGATCAGCGCCAGTGTACTACGACGCGC 666  
 |||||  
 DB 26 GGGGGTTCATGCCACCCAGAGCACTCGGATCATGTGACAGCACTGACAGATTAAC 85  
 |||||  
 QY 667 GGGCGATGAGAGGGGCGCGCCACCTACAGGAGGTCAATCGGCACTACCGGGGTC 726  
 |||||  
 DB 86 GGGAGATGAGAGGGGCGACCCCAATACAGCGAGTGTGGCCACACCGAGCGCC 145  
 |||||  
 QY 727 TCTTTCAGACAGCAGAGAGAGTGGGC 754  
 |||||  
 DB 146 TCTTTCATCATCAGAGCGCAGAACGC 173  
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RESULT 8  
 US-09-902-540-6620  
 ; Sequence 6620, Application US/09902540  
 ; Patent No. 6833447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wiegand, Roger C.  
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902.540  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883

;; PRIOR FILING DATE: 2000-07-10  
;; NUMBER OF SEQ ID NOS: 16825  
;; SEQ ID NO 6620  
;; LENGTH: 645  
;; TYPE: DNA  
;; ORGANISM: Myxococcus xanthus  
US-09-902-540-6620

Query Match 6.6%; Score 57.2; DB 3; Length 645;  
Best Local Similarity 45.7%; Pred. No. 0.0016;  
Matches 200; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 256 TGTGAGGCAACGGAATCCAGAGCCGCAAGTCTACGCCCCGCTCGGCCCAACGACCGC 355  
DB 80 TGGCGGAGCGCGCATCTTGAAAGTGTGAGAGAACCCCTTCTGTCACTTCTTACA 139  
QY 356 TGGCGGTGCGCCCTTGCCTCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTTACCT 415  
DB 140 CGGACCGGAGAGTTCCGGCTTCCAGACGAGATCTTCTTCCGTGTGCGCTTCCGTC 199  
QY 416 ACCCTGACAGAGATGACCTTGACCTTGACCACTTCTGTGACAGCGGAGAGAGCCCC 475  
DB 200 AGCAGCAGAGAGTGTTCAGACGAGACTCTTCAAGCTCGATGACGCTCAAGCACTACT 259  
QY 476 CACCTTACAGAGGCGCCCTGACCTTCCAGCTTCCGAGCCCGAGAGAGCTGGAAGTGA 535  
DB 260 TCGCCAGAGACCGCATCTTTCGCGCATCTCACTGAGCGGACGAGAGCTGCGCTTACG 319  
QY 536 ACCGGAAGTCGCTGCGCGCACCCCAAGAGAACATCTTTCAGACAGTCACTGATGATA 595  
DB 320 AGCGGCTTTCAGAGGCGCTGCGGCGCCCGGCTGCGCAAGCGGACCTGATCTACCTCC 379  
QY 596 GTGCGAGCTGAGCGCGCCCTTGCCTCCAGAGATGATCTGCGCATCAGCGCAAGTGT 655  
DB 380 AGCGCCGACTGAGCGCTCTCTGCAACGATCAAGAGCGCGCGAGATTTCAGCGCA 439  
QY 656 AGCGGACGCGCGGCGCATGAGAGGCGCGCCCGCATCAAGCGAGCTCATCGGCACT 715  
DB 440 AGTTGACCCCAAGTACTGAGAGGCGCTGTCATCTTCAACAACATCTTCTTCACT 499  
QY 716 ACCCGGGTCTCTCTCC 733  
DB 500 ACACGAGACCCCGCTCC 517

RESULT 9  
US-09-902-540-506  
Sequence 506, Application US/09902540  
Patent No. 6833447

;; GENERAL INFORMATION:  
;; APPLICANT: Goldman, Barry S.  
;; APPLICANT: Hinkle, Gregory J.  
;; APPLICANT: Slater, Steven C.  
;; APPLICANT: Wiegand, Roger C.  
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
;; FILE REFERENCE: 38-10(15849)B  
;; CURRENT APPLICATION NUMBER: US/09/902,540  
;; PRIOR FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: 60/217,883  
;; PRIOR FILING DATE: 2000-07-10  
;; NUMBER OF SEQ ID NOS: 16825  
;; SEQ ID NO 506  
;; LENGTH: 2364  
;; TYPE: DNA  
;; ORGANISM: Myxococcus xanthus  
US-09-902-540-506

Query Match 6.6%; Score 57.2; DB 3; Length 2364;  
Best Local Similarity 45.7%; Pred. No. 0.0022;  
Matches 200; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 296 TGTGAGGCAACGGAATCCAGAGCCGAGAGTCTACGCCCCGCTCGGCCCAACGACCGCC 355  
DB 111 TGTGAGGCAACGGAATCCAGAGCCGAGAGTCTACGCCCCGCTCGGCCCAACGACCGCC 355

DB 734 TGGCGGAGCGGCGCATCTCGAAGTGTGAGAGAACCCCTTCTGTCACTTCTTACA 793  
QY 356 TGGCGGTGCGCCCTTGCCTCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTTACCT 415  
DB 794 CGGACCGGAGAGTTCCGGCTTCCAGACGAGATCTTCTTCCGTGTGCGCTTCCGTC 853  
QY 416 ACCCTGACAGAGATGACCTTGACCTTGACCACTTCTGTGACAGCGGAGAGAGCCCC 475  
DB 854 AGCAGCAGAGAGTGTTCAGACGAGACTCTTCAAGCTCGATGACGCTCAAGCACTACT 913  
QY 476 CACCTTACAGAGGCGCCCTGACCTTCCAGCTTCCGAGCCCGAGAGAGCTGGAAGTGA 535  
DB 914 TCGCAGAGACCGCATCTTTCGCGCATCTCAACTGAGAGCGGACGAGAGCTGCGCTTACG 973  
QY 536 ACCGGAAGTCGCTGCGCGCACCCCAAGAGAACATCTTTCAGACAGTGAAGTGA 595  
DB 974 AGCGGCTTTCAGAGGCGCTGCGGCGCCCGGCTGCGCAAGCGGACCTGATCTTACCTCC 1033  
QY 596 GTGCGAGCTGAGCGCGCCCTTGCCTCCAGAGATGATCTGCGCATCAGCGCAAGTGT 655  
DB 1034 AGCGCCGACTGAGCGCTCTCTGCAACGATCAAGAGCGCGCGAGATTTCAGCGCA 1093  
QY 656 AGCGGACGCGCGGCGCATGAGAGGCGCGCCCGCATCAAGCGAGTCACTGCGCACT 715  
DB 1094 AGTTGACCCCAAGTACTGAGAGGCGCTGTCATCTTCAACAACATCTTCTTCACT 1153  
QY 716 ACCCGGGTCTCTCTCC 733  
DB 1154 ACACGAGACCCCGCTCC 1171

RESULT 10  
US-09-902-540-904  
Sequence 904, Application US/09902540  
Patent No. 6833447  
;; GENERAL INFORMATION:  
;; APPLICANT: Goldman, Barry S.  
;; APPLICANT: Hinkle, Gregory J.  
;; APPLICANT: Slater, Steven C.  
;; APPLICANT: Wiegand, Roger C.  
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
;; FILE REFERENCE: 38-10(15849)B  
;; CURRENT APPLICATION NUMBER: US/09/902,540  
;; PRIOR FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: 60/217,883  
;; PRIOR FILING DATE: 2000-07-10  
;; NUMBER OF SEQ ID NOS: 16825  
;; SEQ ID NO 904  
;; LENGTH: 11382  
;; TYPE: DNA  
;; ORGANISM: Myxococcus xanthus  
US-09-902-540-904

Query Match 6.2%; Score 53.2; DB 3; Length 11382;  
Best Local Similarity 47.4%; Pred. No. 0.024;  
Matches 259; Conservative 0; Mismatches 278; Indels 9; Gaps 3;

QY 234 GGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGATGCTGTGAGCTTCCGAGAGCAC 293  
DB 920 GCGGCGGTGAGATGAGAGCTCTGCTCATGAGCCGGGCAACCCGACGATGAGGAGGAA 979  
QY 294 AGTGTGAGGCAACGGAATCCAGAGCCGAGGCTTACAGCCCGCTCGGCCCAACGAGCCG 353  
DB 980 CGGCTCTTCAACCGGACCTGTGTAGCGCGCGGAGAGACGACACAGCGGCCACCTGT 1039  
QY 354 CTTGCGCGTGCAGCCCTTGCCTCCAGCGGAGCGCTTCCAGCGCTTCCAGCCCACTTATCC 413  
DB 1040 CCAAGCCCAAGCGCGGCCCGGAGCGGTACGCTGTGATCAAGTGAAGAGCGC-----GTCC 1095  
QY 414 GTACTGACGACGAGATGACCTTGCACCACTTCTGTGATGACAGCGGAGAGAGCGC 473  
DB 1096 CGGATGAGAGCGCGGAGAAACACAGCAGTAGAGCTTCAGCGCCGCGCATCAGAGCAGCC 1155

QY 474 CCCACCTTACGAGGCCCCCTGCAC--CCTCAGCTTGGGAGCCCCGAGCAGACTGGA 530  
 Db 1156 ACGCCCCACGACGAGAGTGCCTTGGGCTCTTCAAGCGCGGAGCAGACAGGA 1215  
 QY 531 ACTGACCGGAGGTGGTGGCGGACCCCCAAAGAACATCTTCAAGTACTGAT 590  
 Db 1216 A--GAACGCGACGAGAGAGTGCCTCCACGCGCAGCACACCGCACCGCAGCCAC 1273  
 QY 591 GGATAGTCGACGAGTGGGCGGCCCCCTGCACCCAGCAGTAACTCGGAGTACGCGCAC 650  
 Db 1274 GTTCGAGGCGCGCGCGGTACCAAGTACCTCTCTCGGAAGCGAGCAATCATATCAGGAG 1333  
 QY 651 GTGCTACGCGACGCGCGGCGCATGAGGCGCGCGCCCTTACAGTACGAGTATCGG 710  
 Db 1334 GAGCTGCGAGAGCGCGCGGTACGCCACAGCAGAGAGGAGGAGGATCCCCAG 1393  
 QY 711 CCACTACCGCGGCTCTCTCTTCAAGACAGAGAGAGTGGCGCGCTCTTCTGCTGGA 770  
 Db 1394 CCGAGAGAGTGGCGCGGTCCATCAACGCGCGGAATGTCTCCCGCGCGCGCGTGC 1453  
 QY 771 GGGGAC 776  
 Db 1454 CGCGAC 1459

## RESULT 11

US-09-902-540-8567/c  
 ; Sequence 8567, Application US/0902540  
 ; Patent No. 6833447

GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540  
 ; PRIOR FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883  
 ; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 16825  
 ; SEQ ID NO 8567  
 ; LENGTH: 1884  
 ; TYPE: DNA  
 ; ORGANISM: Myxococcus xanthus  
 ; US-09-902-540-8567

Query Match 6.1%; Score 52.6; DB 3; Length 1884;  
 Best Local Similarity 48.0%; Pred. No. 0.022;  
 Matches 213; Conservative 0; Mismatches 226; Indels 5; Gaps 2;

QY 336 GCGTGGGCGCACCGACCGGCTGGCGGCTTGCAGCCGAGGAGGCGCTTCCACG 395  
 Db 1810 GCGAGCACACGCGGCGACCGTCCAGCCCGCCAAAGCGGCGGAGTGCCTGATC 1751  
 QY 396 CTTCACGCCACCTATCTCGTACCTGACGACAGATGACCTTCCACCCACATCTGCT 455  
 Db 1750 AGTGAACACAGCGCGTCCGAGTGAAGCGCGGGAACACACAGCAGTACGCTCAGCG 1691  
 QY 456 GTCAAGCGGAGAGAGCCCCACCTTACGAGGCGCTTGCAC--CCTCAGCTTGGGA 512  
 Db 1690 CCGGCAATCAGAGACAGCAGCGCCCGACGAGCGAGTGCCTTGGTCTCTTCAAGC 1631  
 QY 513 CCGGAGCAGCAGCTGGAATGAACCGGAGTGGTTCGCGCACCCCGCAACAGAACAT 572  
 Db 1630 GCGGAGCAGCAGAGGA--GAACGACAGAGAGAGTGCCTCAGCGCGCAGACACCGC 1573  
 QY 573 CTTCGACAGTACCTGATGATAGTGCAGGCTGGGCGGCGCTTGCCTCCCGCAGAGTAA 632  
 Db 1572 CACCGGAGCAGCAGCAGTGCAGGCGCGCGGTACCAAGTCACTCTCCGGAAGCGA 1513  
 QY 633 CTGGGAGTACAGCGCCAGCTGCTACGAGCGGCGGCGCATGAGAGGCGCGCGCCAC 692

Db 1512 CGCAATCCATATACAGAGAGCTGGAGAGAGCGCGCGGTACCGCCACAGCAGAGAGGC 1453  
 QY 693 CTACAGCAGAGTCAATCGGCACTACCGGAGGTCTCTCTTCCAGACCCAGAGAGAGTGG 752  
 Db 1452 GAGCAGCAGAGGTCTCCACCGCGAGAGAGTGGCGCGGTCCATCAACGCGCGAATGTTC 1393  
 QY 753 GCGGCGCTCTTGTGTGAGGGGAG 776  
 Db 1392 CGCGCGCGCGCGCGGTGGCGCGGAC 1369

## RESULT 12

US-10-104-047-1064

; Sequence 1064, Application US/10104047  
 ; Patent No. 6943241  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: No. 6943241e1 full length cDNA  
 ; FILE REFERENCE: H1-A0105  
 ; CURRENT APPLICATION NUMBER: US/10/104,047  
 ; PRIOR FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER:  
 ; NUMBER OF SEQ ID NOS: 4096  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1064  
 ; LENGTH: 2183  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-104-047-1064

Query Match 5.9%; Score 51; DB 3; Length 2183;  
 Best Local Similarity 46.8%; Pred. No. 0.051;  
 Matches 227; Conservative 0; Mismatches 255; Indels 3; Gaps 2;

QY 313 CCAGAGCCGACAGGTACAGCCCGCGCTCGGCCACCGACCGCTGCGCGCTTTC 372  
 Db 593 CACAGCAGCAGCAGACCCCGACGACGAGCTTCACAGCAGCCCGAGTACGAGCTTGA 652  
 QY 373 GCCCAGCGGAGCGCTTCCAGCGCTTCCAGCCCACTTCTGACTTGCAGCAGAGATC 432  
 Db 653 CAGCAGCAGCAGCAGAGCGCCCGACGAGCAATTCAGTACAGCTTCCAGCAGCAGCAG 712  
 QY 433 GACCTGACCAACCATCTCTGCTTCAGCGGAGAGAGCCCGACCTTACAGGCGCCCG 492  
 Db 713 CCCAGCAGTACCTCCAGCAGCAGCAGCGAGCCCGCAGTACAGCTTCCAGAGCCCTCAG 772  
 QY 493 TGCACCTCAGCTTCCGAGACCCGAGCAGCAGCTGAACTGAACCGGAGTGCCTTC--G 551  
 Db 773 TACAGCTTCAAGCAGCAGCAGCAGCGCCCGCAGTACAGCTTCCAGAGCCCTCAG 832  
 QY 612 CCCCTGCCCCCAGCAGTAACTCGGAGCATCAGCGCACTGTGTAGAGGCGCGGCG 671  
 Db 893 CAGCAGCCCGCAGTACAGCAGCAGCGCCCGCAGTACAGCAGCAGCGCCCGCAGTACAG 952  
 QY 672 CATGAGGAGCGCGCGCCCGACCTTACAGAGGTATCGGCACTACCCGAGGCTCTTC-- 729  
 Db 953 CAGCAGAGCCCGACCGCCCGTACAGCAGCGCCCGCAGCAGCAGCAGCTTCCAGCAGCAG 1012  
 QY 730 TTCAGCAGCAGCAGCAGTGGCGCGCTCTTCTTGTGAGGAGGACCGGCTTCACAC 789  
 Db 1013 TCCACAGCAGCAGAGTCCAGCAGCAGCAGTCCAGCAGCAGCGCCCGCAGCAGCTTG 1072  
 QY 790 ACACA 794  
 Db 1073 CCGCA 1077

## RESULT 13

US-09-949-016-3915  
; Sequence 3915, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3915  
; LENGTH: 1122  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-3915

Query Match 5.8%; Score 50.2; DB 3; Length 1122;  
Best Local Similarity 47.7%; Pred. No. 0.066;  
Matches 179; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

QY 323 AGGTCTAGCCGCCGCTCGCCGACCGACCGCTGGCCGCTTCCGCCACGGG 382  
DB 306 AGTTGCCCCCTGTGCCCCGGGAGACCCCGGCGCCGACGTCGCAAGTACGGGCTGC 365  
QY 383 AGCGCTTCACCGCTTCGAGCCCACTATCCGTACTGACGACGAGATGCACTGCCAC 442  
DB 366 CGGGGCTGGCGAGCTCAAGACCGCGAGTCGTAAGTGTGCTGCTA---CGACCGCGCA 422  
QY 443 CCACCATCTCGGTGTCAAGACGGGAGAGCCGCCACCTTACAGGGGCCCTGCAACCTCC 502  
DB 423 CCGCGCGCGCTCTGAGTGTGAGAGCTGCGACCCGAGGTCTCCGCGCGAGGCG 482  
QY 503 AGCTTCGGGACCCCGAGCAGACTGGAATGAAACCGGAGTGTGCGGACCCCA 562  
DB 483 ACCGGGCGAGTGCAGCTTCCGAGAGAGACGTCGGTGAACGATACCAACGTCACACA 542  
QY 563 ACAGAACCATCTTCGACAGTGAACCTGATGATAGTCCAGGCTGGGCGCCCTGCCCC 622  
DB 543 AGCGGCACTACGCGCGGAGTGGCTTGAACCGCGTCACTGGCGCGCGCCCAACCAAC 602  
QY 623 CCAGCAGTAACTCGGGCATCAGCGCCAGTGTGCTACGCGGCGGGGCCCATGAGGGGC 682  
DB 603 GCTGAGCCAGAGGCGCATGAGCAGACGTTCTACCTGAGCAACGTGCGGCCCAAGTGC 662  
QY 683 CGCCGCCCACTTACA 697  
DB 663 CCCACTCAACCA 677

RESULT 14  
US-09-252-991A-13687  
; Sequence 13687, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27.  
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 13687  
; LENGTH: 696  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13687

Query Match 5.6%; Score 48; DB 3; Length 696;  
Best Local Similarity 57.2%; Pred. No. 0.18;  
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACCGAGCTGAGTTGTTCAGATCATCATCTGCTGTGATGATGATGATGATG 168  
DB 482 ACCCTGTAACCTTCTGTTGCGATCGTCCGCGGGGTGCTGCGGCTGCTG 541  
QY 169 GTGATCAGTGTCTGCTGAGCACTACAAAGCTGTGACGCTCTTATACGCCGAC 228  
DB 542 CTGTCAAGCCGCTGCTGCGCAAGAAAGAAAGACTGAGCTGACCTGACCTGCGCGAG 601  
QY 229 AGCCAGGGCGGAGAGAGAGATGCCCTGTC 260  
DB 602 CGCATTCGCGAGGCGGATGACCGCCCTGCG 633

RESULT 15  
US-09-252-991A-13650/C  
; Sequence 13650, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13650  
; LENGTH: 1452  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13650

Query Match 5.6%; Score 48; DB 3; Length 1452;  
Best Local Similarity 57.2%; Pred. No. 0.22;  
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACCGAGCTGAGTTGTTCAGATCATCATCTGCTGTGATGATGATGATGATG 168  
DB 267 ACCCTGTAACCTTCTGTTGCGATCGTCCGCGGGGTGCTGCGGCTGCTG 208  
QY 169 GTGATCAGTGTCTGCTGAGCACTACAAAGCTGTGACGCTCTTATACGCCGAC 228  
DB 207 CTGTCAAGCCGCTGCTGCGCAAGAAAGAAAGACTGAGCTGACCTGACCTGCGCGAG 148  
QY 229 AGCCAGGGCGGAGAGAGAGATGCCCTGTC 260  
DB 147 CGCATTCGCGAGGCGGATGACCGCCCTGCG 116

Search completed: February 28, 2006, 12:29:27  
Job time: 176.41 secs



Db 181 CTGCTGAGCCTACTAAGCTGTCTGACAGGCTCTTCATTCAGCCGGCAGACAGCGGGGG 240  
Qy 241 AGGAGAGAAAGATGCTCTGTCTCTCAAGAGATGCTGTGGCCCTCGAGAGACAGCTGTCA 300  
Db 241 AGGAGAGAAAGATGCTCTGTCTCTCAAGAGATGCTGTGGCCCTCGAGAGACAGCTGTCA 300  
Qy 301 GGCAAGAGAAATCCGAGAGCCGAGAGCTTACGCGCCCGCTCGGAGCCGAGCCGCTGGCC 360  
Db 301 GGCAAGAGAAATCCGAGAGCCGAGAGCTTACGCGCCCGCTCGGAGCCGAGCCGCTGGCC 360  
Qy 361 GTGCGGCTCTTGGCCAGCGGAGAGGCTTCAACCGCTTCAGCCCACTATCCGTAAGTCC 420  
Db 361 GTGCGGCTCTTGGCCAGCGGAGAGGCTTCAACCGCTTCAGCCCACTATCCGTAAGTCC 420  
Qy 421 CAGCAGAGATGAGCTGCTGACCCCAACATCTGCTGTGAGAGCGGGAGAGGCCCCACCC 480  
Db 421 CAGCAGAGATGAGCTGCTGACCCCAACATCTGCTGTGAGAGCGGGAGAGGCCCCACCC 480  
Qy 481 TACAGAGGCTCTGACCTCTCAAGCTTGGGAGACCCGAGACAGAGTGAATGAACCGG 540  
Db 481 TACAGAGGCTCTGACCTCTCAAGCTTGGGAGACCCGAGACAGAGTGAATGAACCGG 540  
Qy 541 GAGTGGTGGCGGACCCCAAGAAACATCTTCAAGTGAACCTGATGATAGTGC 600  
Db 541 GAGTGGTGGCGGACCCCAAGAAACATCTTCAAGTGAACCTGATGATAGTGC 600  
Qy 601 AGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 AGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Qy 661 AACGGGCGGCGATGAGAGGGGCGCGCCCACTTAAAGAGAGTCACTGAGCACTAACCGG 720  
Db 661 AACGGGCGGCGATGAGAGGGGCGCGCCCACTTAAAGAGAGTCACTGAGCACTAACCGG 720  
Qy 721 GGGTCTCTCTTCCAGACCAAGAGAGAGTGGGCGCGCTCTGCTGAGAGGAGAGCCCG 780  
Db 721 GGGTCTCTCTTCCAGACCAAGAGAGAGTGGGCGCGCTCTGCTGAGAGGAGAGCCCG 780  
Qy 781 CTCACACACACACATGCGGCTCTGAGAGAGGAGAGTGAAGTGAAGTGAAGTGAAGT 840  
Db 781 CTCACACACACACATGCGGCTCTGAGAGAGGAGAGTGAAGTGAAGTGAAGTGAAGT 840  
Qy 841 AAACAGAAAGACACCTCTC 861  
Db 841 AAACAGAAAGACACCTCTC 861

RESULT 2  
US-10-295-027-127  
Sequence 127, Application US/10295027  
GENERAL INFORMATION:  
APPLICANT: Afari, Daniel  
APPLICANT: Aziz, Natesha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Ros Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15

Qy PRIOR APPLICATION NUMBER: US 60/332,464  
Db PRIOR FILING DATE: 2001-11-21  
Qy PRIOR APPLICATION NUMBER: US 60/334,393  
Db PRIOR FILING DATE: 2001-11-29  
Qy PRIOR APPLICATION NUMBER: US 60/340,376  
Db PRIOR FILING DATE: 2001-12-14  
Qy PRIOR APPLICATION NUMBER: US 60/347,211  
Db PRIOR APPLICATION NUMBER: US 60/347,349  
Qy PRIOR FILING DATE: 2002-01-10  
Db PRIOR APPLICATION NUMBER: US 60/355,250  
Qy PRIOR FILING DATE: 2002-02-08  
Db PRIOR APPLICATION NUMBER: US 60/356,714  
Qy PRIOR FILING DATE: 2002-02-13  
Db Remaining Prior Application data removed - See File Wrapper or PALM.  
Qy NUMBER OF SEQ ID NOS: 1386  
Db SOFTWARE: Patent In Ver. 2.1  
Qy SEQ ID NO 127  
Db LENGTH: 864  
Qy TYPE: DNA  
Db ORGANISM: Homo sapiens  
Qy US-10-295-027-127  
Db

Query Match 100.0%; Score 861; DB 6; Length 864;  
Best Local Similarity 100.0%; Pred. No. 1,5e-219; Mismatches 0; Gaps 0;  
Matches 861; Conservative 0; Indels 0; Gaps 0;

Qy 1 ATGACCGCTTGTATGAGGAGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Db 1 ATGACCGCTTGTATGAGGAGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Qy 61 TCTTCAGAGTGAATGAGAAAGCTCTTGTTCAGAGAGAGAGATGAGAGAGAGAGAGAGAGAG 120  
Db 61 TCTTCAGAGTGAATGAGAAAGCTCTTGTTCAGAGAGAGAGATGAGAGAGAGAGAGAGAGAG 120  
Qy 121 TTTGTTCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180  
Db 121 TTTGTTCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180  
Qy 181 CTGCTGAGCACTAAGAGTGTCTGACAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
Db 181 CTGCTGAGCACTAAGAGTGTCTGACAGGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
Qy 241 AGGAGAGAAAGTCCCTTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
Db 241 AGGAGAGAAAGTCCCTTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
Qy 301 GGCAAGAGAAATCCGAGAGCCGAGAGCTTACGCGCCCTCGGAGAGAGAGAGAGAGAGAGAG 360  
Db 301 GGCAAGAGAAATCCGAGAGCCGAGAGCTTACGCGCCCTCGGAGAGAGAGAGAGAGAGAGAG 360  
Qy 361 GTGCGGCTCTTGGCCAGCGGAGAGGCTTCAACCGCTTCAGCCCACTATCCGTAAGTCC 420  
Db 361 GTGCGGCTCTTGGCCAGCGGAGAGGCTTCAACCGCTTCAGCCCACTATCCGTAAGTCC 420  
Qy 421 CAGCAGAGATGAGCTGCTGACCCCAACATCTGCTGTGAGAGCGGGAGAGGCCCCACCC 480  
Db 421 CAGCAGAGATGAGCTGCTGACCCCAACATCTGCTGTGAGAGCGGGAGAGGCCCCACCC 480  
Qy 481 TACAGAGGCTCTGACCTCTCAAGCTTGGGAGACCCGAGACAGAGTGAATGAACCGG 540  
Db 481 TACAGAGGCTCTGACCTCTCAAGCTTGGGAGACCCGAGACAGAGTGAATGAACCGG 540  
Qy 541 GAGTGGTGGCGGACCCCAAGAAACATCTTCAAGTGAACCTGATGATAGTGC 600  
Db 541 GAGTGGTGGCGGACCCCAAGAAACATCTTCAAGTGAACCTGATGATAGTGC 600  
Qy 601 AGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 AGGCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Qy 661 AACGGGCGGCGATGAGAGGGGCGCGCCCACTTAAAGAGAGTGAAGTGAAGTGAAGTGAAGT 720  
Db 661 AACGGGCGGCGATGAGAGGGGCGCGCCCACTTAAAGAGAGTGAAGTGAAGTGAAGTGAAGT 720

Db	773	GTGCGCCCTTCCGCCAGCGGGAGCGCTTCAACGGCTTCAGGCCACCTATCCGTACTGG	83.2
QY	421	CAGCAGAGATGCACCTGCCACCCACCATTCTGCTGTCAAGCGGGGAGGAGCCCCCAACC	480
Db	833	CACACACAGATTCACCTGCGCACCCACCACTTGTGTGACAGCGGAGAGCCCCCAACC	892
QY	481	TACAGAGGCCCCCTGCAACCTTCAGCTTCGGGACCCCGAGAGCAGCTTGAACTTGAACCGG	540
Db	893	TACAGAGGCCCCCTGCAACCTTCAGCTTCGGGACCCCGAGAGCAGCTTGAACTTGAACCGG	952
QY	541	GAGTCGGTGCAGCACTCCCAACAGAACATCTTTCACAGTGAACCTGATGATATGAGCC	600
Db	953	GAGTCGGTGCAGCACTCCCAACAGAACATCTTTCACAGTGAACCTGATGATATGAGCC	1012
QY	601	AGGCTGGGGGGCCCCCTGSCCCCCCAGAGATTACTCGGGCATCAAGCGCACTGTCTACGGC	660
Db	1013	AGGCTGGGGGGCCCCCTGSCCCCCCAGAGATTACTCGGGCATCAAGCGCACTGTGTACGGC	1072
QY	661	AGCGCGGGGCGCATGAGGGGCGCGCGCCACCTTACAGCGAGTCACTCGCCACTTACCCG	720
Db	1073	AGCGCGGGGCGCATGAGGGGCGCGCGCCACCTTACAGCGAGTCACTCGCCACTTACCCG	1132
QY	721	GGGTCCTCTTTCACAGCAACAGAGAGATGGGCGCGCTCTCTTGTGAGGGGACCCGG	780
Db	1133	GGGTCCTCTTTCACAGCAACAGAGAGATGGGCGCGCTCTCTTGTGAGGGGACCCGG	1192
QY	781	CTCCACCAACAACATCGCGCCCCCTTGAAGGCGAGCCATCTGGAGCAAAAGAGAGAT	840
Db	1193	CTCCACCAACAACATCGCGCCCCCTTGAAGGCGAGCCATCTGGAGCAAAAGAGAGAT	1252
QY	841	AAACAGAAAGAGCACTCTTC	861
Db	1253	AAACAGAAAGAGCACTCTTC	1273

```

RESULT 4
US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantcz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-119

Query Match          100.0%; Score 861; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 1,9e+219;
Matches      861; Conservative    0; Mismatches    0; Indels    0; Gaps    0

        1 ATGCACCGCTTGATGGGAGTCAACGACGCCGCCGCCGCCGCCGCGGAGCCCAATGTTC   60
Db       321 ATGCACCGCTTGATGGGAGTCAACGACGCCGCCGCCGCCGCCGCGGAGCCCAATGTTC   380

QY       61 TCCTGCACGTGCAACTGCAAAAGCCTCTTTGTTCCAGACATAGAGATACCGAGCTGGAG   120
DB       381 TCCTGCACGTGCAACTGCAAAAGCCTCTTTGTTCCAGACATAGAGATACCGAGCTGGAG   440
QY       121 TTGTGTCAGATCATCATCATGCTGGTGGTAGTAGAGTAGAGTAGGTGGTGGTAGTCAGCTGC   180

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Best Local Similarity 100.0%; Pred. No. 1.9e-219;  
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACCCGCTTATGAGGGGATCAAGACACCGCCGCGCGCCGCGGAGCCCATGTC 60  
DB 321 ATGACCCGCTTATGAGGGGATCAAGACACCGCCGCGCGCGCGGAGCCCATGTC 380  
QY 61 TCTGACGTCGAACTGAAAGCTCTTTTGTTCAGAGAGATGAGATCAAGAGTGGAG 120  
DB 381 TCTGACGTCGAACTGAAAGCTCTTTTGTTCAGAGAGATGAGATCAAGAGTGGAG 440  
QY 121 TTTTGTTCAGATCATATCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 180  
DB 441 TTTTGTTCAGATCATATCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 500  
QY 181 CTGCTGACGTCATCAAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 240  
DB 501 CTGCTGACGTCATCAAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 560  
QY 241 AGGAGAGAGATGTCCTGTCCTCAGAGAGATGTCCTGTCCTGTCCTGTCCTGTCCT 300  
DB 561 AGGAGAGAGATGTCCTGTCCTCAGAGAGATGTCCTGTCCTGTCCTGTCCTGTCCT 620  
QY 301 GCGACGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360  
DB 621 GCGACGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 680  
QY 361 GTGCGGCTTGTGCGCGAGGAGGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCG 420  
DB 681 GTGCGGCTTGTGCGCGAGGAGGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCG 740  
QY 421 CAGCAGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480  
DB 741 CAGCAGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 800  
QY 481 TACCGAGGCTTGTGCGCGAGGAGGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCG 540  
DB 801 TACCGAGGCTTGTGCGCGAGGAGGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCG 860  
QY 541 GAGTGGGTCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 600  
DB 861 GAGTGGGTCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 920  
QY 601 AGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660  
DB 921 AGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 980  
QY 661 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
DB 981 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1040  
QY 721 GGGTCTCTCTTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 780  
DB 1041 GGGTCTCTCTTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1100  
QY 781 CTCAC 840  
DB 1101 CTCAC 1160  
QY 841 AAACAGAAAGACACCTCTTC 861  
DB 1161 AAACAGAAAGACACCTCTTC 1181

RESULT 10  
US-09-796-753-55  
; Sequence 55, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796, 753

CURRENT FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: 09/183,175  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 09/223,094  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/223,546  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/224,246  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/259,388  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/122,458  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: 09/312,359  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/336,536  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 09/342,687  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 09/345,464  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/365,164  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 09/399,723  
PRIOR FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: 09/409,634  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 09/471,179  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 09/474,071  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/474,072  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/514,010  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 09/516,745  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 09/572,002  
PRIOR FILING DATE: 2000-05-14  
PRIOR APPLICATION NUMBER: 09/597,993  
PRIOR FILING DATE: 2000-06-19  
PRIOR APPLICATION NUMBER: 09/599,596  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 09/630,334  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: 09/606,565  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/606,317  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/665,666  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: 09/677,751  
PRIOR FILING DATE: 2000-09-30  
NUMBER OF SEQ ID NOS: 162  
SEQ ID NO 55  
LENGTH: 969  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (6)...(761)  
US-09-796-753-55

Query Match 87.7%; Score 755.2; DB 3; Length 969;  
Best Local Similarity 99.6%; Pred. No. 2.5e-191;  
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 GGAGATCAGGAGCTGAGGCTTTTTCATATCATATCATATCATATCATATCATATCATATCATAT 161  
DB 2 GGAGATGCGGAGCTGAGGCTTTTTCATATCATATCATATCATATCATATCATATCATATCATAT 61  
QY 162 GGTGTGTGTATCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 221







Db	197	ACGGTCCTTCATCAGCCGGGACAGCGACAGGGGGCGAGAGAGAAAGATGCCCTGTCTCAG	256
QY	267	AGGATGCTGTGGGCCCTCGAGAGACACAGTGTCAAGCAA	326
Db	257	AGGATGCTGTGGGCCCTCGAGAGACACAGTGTCAAGCAA	316
QY	327	CTAGCGCCCGGCTCGGACCCAGACCGACCGCTGGCGCGCTTTCGCGCAGGGAGCG	386
Db	317	CTAGCGCCCGGCTCGGACCCAGACCGACCGCTGGCGCGCTTTCGCGCAGGGAGCG	376
QY	387	CTTCCACCGCTTTCAGGCCACCTATCCGTA	446
Db	377	CTTCCACCGCTTTCAGGCCACCTATCCGTA	436
QY	447	CATCGCGTGTCAAGCGGGAGAGAGCCGCCACCCCTACAGAGGCCCCCTGCACTCCAGCT	506
Db	437	CATCGCGTGTCAAGCGGGAGAGAGCCGCCACCCCTACAGAGGCCCCCTGCACTCCAGCT	496
QY	507	TCGGGACCCCGAGGACGACGCTGAACTGAA	566
Db	497	TCGGGACCCCGAGGACGACGCTGAACTGAA	556
QY	567	AACCATCTTTCGACACTGACCTGATGATGATGACGAGGCTGGGGGGCCCTGCCCCCAG	626
Db	557	AACCATCTTTCGACACTGACCTGATGATGATGACGAGGCTGGGGGGCCCTGCCCCCAG	616
QY	627	CAGTAACTCGGGACATCAACCGCACCTGTGCTACCGGACGGCGGCGCATGAGAGGGCGCC	686
Db	617	CAGTAACTCGGGACATCAACCGCACCTGTGCTACCGGACGGCGGCGCATGAGAGGGCGCC	676
QY	687	GCCCACTTACAGCGAGGTCATGCGGCACTACCCGGGGTCTCTTTCAGACACAGACAG	746
Db	677	GCCCACTTACAGCGAGGTCATGCGGCACTACCCGGGGTCTCTTTCAGACACAGACAG	736
QY	747	CAGTGGGCGCGCCTCTTGTGAGAGGAGCCCGGCTCCACACACACATGCGCGCCCT	806
Db	737	CAGTGGGCGCGCCTCTTGTGAGAGGAGCCCGGCTCCACACACACATGCGCGCCCT	796
QY	807	AGAGAGCGCAGGCATCTGAGCAAGCAAGAGATTAACGAAAGGACACCTCTC	861
Db	797	AGAGAGCGCAGGCATCTGAGCAAGCAAGAGATTAACGAAAGGACACCTCTC	851
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US-10-241-220-44			
; Sequence 44, Application US/10241220			
; Publication No. US20030148408A1			
; GENERAL INFORMATION:			
; APPLICANT: Frantz, Gretchen			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Phillips, Heidi			
; APPLICANT: Polakis, Paul			
; APPLICANT: Spencer, Susan			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wu, Thomas			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
; TITLE OF INVENTION: TREATMENT OF TUMOR			
; FILE REFERENCE: P5010R1-US			
; CURRENT APPLICATION NUMBER: US/10/241,220			
; CURRENT FILING DATE: 2002-12-13			
; NUMBER OF SEQ ID NOS: 120			
; SEQ ID NO 44			
; LENGTH: 1850			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-241-220-44			

Query Match	87.6%	Score 754.2	DB 6	Length 1850
Best Local Similarity	98.3%	Pred. No. 5,1e-191		
Matches 762; Conservative	0;	Mismatches 13;	Indels	0;
			Gaps	0

QY	87	TTTGTTCCAGACACATGAGAGATCAAGCAAGCACTGGAAGTTTGTTCAGATCATCATCATCGTGT	146
Db	77	TTCTCCGCAAAACAGGCAATGGCGGACTGGAAGTTTGTTCAGATCATCATCATCGTGT	136
QY	147	GGTATGATGATGATGATGATGATGATGATCACTGCTCTGAGCCATCAAGCTGTCTGC	206
Db	137	GGTATGATGATGATGATGATGATGATGATCACTGCTCTGAGCCATCAAGCTGTCTGC	196
QY	207	ACGTCCTTCATCAAGCCGCGACAGCCAGGGCGGAGAGAAAGATGCCGTGCTCAGA	266
Db	197	ACGTCCTTCATCAAGCCGCGACAGCCAGGGCGGAGAGAAAGATGCCGTGCTCAGA	256
QY	267	AGGATGCTGTGGGCGCTCGAGAGACAGAGTGCAGGCAACGGAAATCCAGAGCCGACAGT	326
Db	257	AGGATGCTGTGGGCGCTCGAGAGACAGAGTGCAGGCAACGGAAATCCAGAGCCGACAGT	316
QY	327	CTAACGCCCCGCGCTCGGCGCCACCGAACCGCTGGCGGTGCGCGCTTTCGCGCCAGCGGAGCG	386
Db	317	CTAACGCCCCGCGCTCGGCGCCACCGAACCGCTGGCGGTGCGCGCTTTCGCGCCAGCGGAGCG	376
QY	387	CTTTCACACGCTTTCAGGCCCACTTATCCGTACTTGAGAGACAGATTCGACTGTGCCACCCAC	446
Db	377	CTTTCACACGCTTTCAGGCCCACTTATCCGTACTTGAGAGACAGATTCGACTGTGCCACCCAC	436
QY	447	CATCTGCTGTAGAGACGGGAGAGACCCGCCACCTGACAGAGGGCCCTGCACCTCCAGCT	506
Db	437	CATCTGCTGTGTAGAGACGGGAGAGACCCGCCACCTGACAGAGGGCCCTGCACCTCCAGCT	496
QY	507	TGCGGACCCCGAGCAGCACTGGAATGTAAACCGGAGAGTCGGTGGCGGCAACCCCAACAG	566
Db	497	TGCGGACCCCGAGCAGCACTGGAATGTAAACCGGAGAGTCGGTGGCGGCAACCCCAACAG	556
QY	567	AACCATCTTTCAGACATGACCTTGATGATATGATGCCAGGCTGGGCGGCGCCCTGCCCCCAG	626
Db	557	AACCATCTTTCAGACATGACCTTGATGATATGATGCCAGGCTGGGCGGCGCCCTGCCCCCAG	616
QY	627	CAGTAACTGGGGCATAGCGCCACGTCGTAACGCGCAGCGCGGGGCGATATGAGGGGGCGGC	686
Db	617	CAGTAACTGGGGCATAGCGCCACGTCGTAACGCGCAGCGCGGGGCGATATGAGGGGGCGGC	676
QY	687	GGCCACCTACAGGAGAGTCAATCGGCACCTACCCGGGGTCTCTCTTCCAGCACACGACAG	746
Db	677	GGCCACCTACAGGAGAGTCAATCGGCACCTACCCGGGGTCTCTCTTCCAGCACACGACAG	736
QY	747	CAGTGGGCGGCGCTCTTGTCTGAGGGGACCCGGCTCCACACACACATCGCGCCCT	806
Db	737	CAGTGGGCGGCGCTCTTGTCTGAGGGGACCCGGCTCCACACACACATCGCGCCCT	796
QY	807	AGAGACGCGACGCATCTGGAGCAAAAGAAAGGATAAACAGAAAGGACCCCTTC	861
Db	797	AGAGACGCGACGCATCTGGAGCAAAAGAAAGGATAAACAGAAAGGACCCCTTC	851

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RESULT 15
US-10-872-972-44
; Sequence 44, Application US/10872972
; Publication No. US20040229277A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,972
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 28, 2006, 09:34:50 / Search time 1128.53 Seconds  
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1626.862 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861  
Sequence: 1 atgcacgcctgatgsgggc.....aacagaagaacaccccttc 861

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications\_NA\_New.\*  
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11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*  
12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq4.\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754.2	87.6	1141	12	US-11-186-284-208
2	87.6	10.2	94	8	US-10-310-914A-1106
3	80	9.3	129	8	US-10-310-914A-7163
4	64	7.4	97	8	US-10-310-914A-6542
5	62.4	7.2	97	8	US-10-310-914A-1107
6	61.4	7.1	63	8	US-10-310-914A-7162
7	51	5.9	2183	9	US-11-072-512-1064
8	45.6	5.3	2561	12	US-11-127-877-26
9	44.6	5.2	200628	12	US-11-121-086-62
10	44.2	5.1	11070	12	US-11-075-185-34
11	44.2	5.1	78869	12	US-11-075-185-1
12	44.2	5.1	2226	12	US-11-052-554A-545
13	43.4	5.0	646	6	US-09-925-065A-607564
14	43.4	5.0	2736	8	US-10-858-730-38
15	43.2	5.0	7402	8	US-10-750-185-27313
16	43.2	5.0	7402	8	US-10-750-623-27313
17	43	5.0	1088	6	US-09-925-065A-69151
18	42.6	4.9	8831	7	US-10-412-748-12
19	42.6	4.9	9729	7	US-10-412-748-10
20	42.2	4.9	2257	8	US-10-770-726-16

21	42	4.9	88421	12	US-11-205-109-1	Sequence 1, Appl
22	41.6	4.8	172111	12	US-11-121-086-28	Sequence 28, Appl
23	41.4	4.8	463	6	US-09-925-065A-213874	Sequence 213874, A
24	41	4.8	379	6	US-09-925-065A-71692	Sequence 71692, A
25	40.8	4.7	1662	12	US-11-136-619-3	Sequence 3, Appl
26	40.8	4.7	1986	12	US-11-183-136-5	Sequence 5, Appl
27	40.8	4.7	17112	12	US-11-176-253-2	Sequence 2, Appl
28	40.6	4.7	577	6	US-09-925-065A-119552	Sequence 119552, A
29	40.6	4.7	3426	12	US-11-136-527-2427	Sequence 2427, Ap
30	40.4	4.7	2276	8	US-10-131-826A-9	Sequence 9, Appl
31	40.2	4.7	201	12	US-11-124-368A-15273	Sequence 15273, A
32	40.2	4.7	2479	12	US-11-136-527-3303	Sequence 3303, Ap
33	40.2	4.7	4598	8	US-10-955-054A-71	Sequence 71, Appl
34	40.2	4.7	150468	12	US-11-112-908-56	Sequence 56, Appl
35	40.2	4.7	193789	12	US-11-112-908-55	Sequence 55, Appl
36	40	4.6	1928	12	US-11-012-668-15	Sequence 15, Appl
37	39.8	4.6	554	6	US-09-925-065A-408177	Sequence 408177, A
38	39.8	4.6	600	8	US-10-750-185-19533	Sequence 19533, A
39	39.8	4.6	600	8	US-10-750-623-19533	Sequence 19533, A
40	39.6	4.6	98345	12	US-11-112-908-35	Sequence 35, Appl
41	39.6	4.6	127340	12	US-11-112-908-35	Sequence 35, Appl
42	39.4	4.6	2515	12	US-11-136-527-2896	Sequence 2896, Ap
43	39.4	4.6	114801	12	US-11-121-086-22	Sequence 22, Appl
44	39.2	4.6	772	6	US-09-925-065A-934808	Sequence 934808, A
45	39.2	4.6	1666	12	US-11-136-527-336	Sequence 336, App

## ALIGNMENTS

RESULT 1  
US-11-186-284-208  
Sequence 208, Application US/11186284  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kametkar, Shubhangi  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Thibodeau, Stephen N.  
APPLICANT: Burgart, Lawrence J.  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF COLON CANCER  
FILE REFERENCE: MP01-0292PRM  
CURRENT APPLICATION NUMBER: US/11/186,284  
CURRENT FILING DATE: 2005-07-21  
PRIOR APPLICATION NUMBER: US/10/301,822  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 208  
LENGTH: 1141  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (96)....(854)  
US-11-186-284-208  
Query Match 87.6%; Score 754.2; DB 12; Length 1141;  
Best Local Similarity 98.3%; Pred. No. 1.6e-168;  
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
87 TTGTTCAGAGCATGAGATCATCGAGCTGGAGTTTTCAGATCATCATCTGTGT 146





Oy 790 ACACA 794  
Db 1073 CCCCA 1077

## RESULT 8

US-11-127-877-26/c  
; Sequence 26, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spittaels, Koenraad F. F.  
; APPLICANT: Laenen, Wendy  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; TITLE OF INVENTION: Methods and Compound Assays For Inhibiting  
; FILE REFERENCE: P27,800-B USA  
; CURRENT APPLICATION NUMBER: US/11/127,877  
; PRIOR FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,352  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: 60/603,948  
; PRIOR FILING DATE: 2004-08-24  
; NUMBER OF SEQ ID NOS: 590  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26  
; LENGTH: 2561  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-127-877-26

Query Match 5.3%; Score 45.6; DB 12; Length 2561;

Best Local Similarity 46.3%; Pred. No. 0.15;  
Matches 150; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

Oy 454 CTGTGACAGCGGGAGAGAGCCCACTTACAGAGGCGCCCTGACCCCTCCAGCTTGGGAC 513  
Db 2082 CTGCTGTGAGGCGGCGCTGCTGCGGTAAGTCCCTGCGGCGCATGGCGCCCGCTC 2023  
Oy 514 CCCGACGACGAGCTGAACTGAACCGGAGTGTGTCGCGGCAACCCCAACGAACATC 573  
Db 2022 TTGTGCGCGCGCGCGGCGGCGGACGACGCGCTGTGAACCGCGCACGACTCCACC 1963  
Oy 574 TTGACAGTGAAGTATGATGATGACGAGGCTGGGGCGGCCCTGCCCCCAGCAGTAC 633  
Db 1962 GCTTGGCCGACCAATCCAGCGCCGACGATGATCCACACGAGGACATGAATAC 1903  
Oy 634 TCGGACATCAGCGGACGCTGTAAGGACGCGGCGGCGGATGAGAGGCGCGCCGAC 693  
Db 1902 TTGACATGAGACCCAGTACTCGGCTTGGCGGCGGCTGCGGCTGCTGCGGCGG 1843  
Oy 694 TACAGCAGGTATGAGGACCTACCGGGGCTCTCTTCCAGACACAGAGAGTGG 753  
Db 1842 CAGGCGAGGTAGGCGCGCTCCAGCTCTGCGGTGTGTCTGTCTGTACAGTACG 1783  
Oy 754 CCGCCCTCTTGTGAGGAGAC 777  
Db 1782 GCCACCAATGCTGCGGAGAC 1759

## RESULT 9

US-11-121-086-62/c  
; Sequence 62, Application US/11121086  
; Publication No. US2005026459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138, 6000-0000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; PRIOR FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 62  
; LENGTH: 200628  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-62

Query Match 5.2%; Score 44.6; DB 12; Length 200628;

Best Local Similarity 65.7%; Pred. No. 0.35;  
Matches 65; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Oy 89 TGTTCAGAGCATGAGATGACGAGCTGAGATTGTTGATCATCATCATCGTGGTGG 148  
Db 129693 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 129634  
Oy 149 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187  
Db 129633 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 129595

## RESULT 10

US-11-075-185-34  
; Sequence 34, Application US/11075185  
; Publication No. US20050266434A1  
; GENERAL INFORMATION:  
; APPLICANT: REYES, CHRISTOPHER D  
; APPLICANT: JULIEN, BRYAN  
; APPLICANT: REID, RALPH  
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS  
; FILE REFERENCE: 010099.03  
; CURRENT APPLICATION NUMBER: US/11/075,185  
; PRIOR FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/551,103  
; PRIOR FILING DATE: 2004-03-08  
; PRIOR APPLICATION NUMBER: US 60/568,290  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 34  
; LENGTH: 11070  
; TYPE: DNA  
; ORGANISM: Sorangium cellulosum  
US-11-075-185-34

Query Match 5.1%; Score 44.2; DB 12; Length 11070;

Best Local Similarity 43.9%; Pred. No. 0.35;  
Matches 190; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

Oy 386 GCTTCCACCGCTTCAGCCCACTATCCGTACTGACAGACAGATGACCTGCCACCA 445  
Db 7001 GCGCGCGCGGCGAGATGCTGCTCCGAGCGCGCTCGGAGCGCGGCTTGTCTCCA 7060  
Oy 446 CCATCTGCTGTGACAGCGGAGAGAGCCCACTTACAGAGGCGCTTGCACCTCGAGC 505  
Db 7061 GCTTCCGCAAGACGAGAGGCGCTCGCTTGTGACAGCGCGCTGCGGCTGATG 7120  
Oy 506 TTGCGAGACCCGAGACAGTGAATGAACCGGAGTGTGTGCGGACCCCAACA 565  
Db 7121 TACGCGACACGCCCTGACCTGCTGCTTGTGACGACCGGCGCGCGCGCTG 7180  
Oy 566 GAACCATCTTGAAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATG 625  
Db 7181 AGCTGCCACTTATGCTTCCAGGACGAGCTTATGCTTCCAGGCGCCGAGGCTTGC 7240  
Oy 626 GCACTAATCGGAGCATGAGCGGACGCTTACAGGACGAGCGGCGGATGAGAGGCGC 685  
Db 7241 CCAAGCTGAGGAGGCTTGTGCTACCGCGGAAACACCAATGAGCTGTGAGCGCTCC 7300  
Oy 686 CGCCACCTTACAGGAGGTATGAGGCACTAACCGGAGTCTCTTCCAGACCAAGACA 745  
Db 7301 GCTTGGGACCGGAGTGTGATGCTTCTGAGCGGCGCGCTTCCACAGGACCAACCGT 7360

Qy 746 GCAAGTGGCCGCTCTTCTGAGAGGAGCCGGCTCCACCAACACATCGGCC 805  
Db 7361 GGGTCTCGACACACGTGGCTGGGACGCGCTGCTCCGGGACCGGCTTCGTGAGC 7420  
Qy 806 TAGAGAGCGCAGC 818  
Db 7421 TGGGCTGGGCGGC 7433

## RESULT 11

US-11-075-185-1  
; Sequence 1, Application US/11075185  
; Publication No. US2005026434A1  
; GENERAL INFORMATION:  
; APPLICANT: REEVES, CHRISTOPHER D  
; APPLICANT: JULIEN, BRYAN  
; APPLICANT: REID, RALPH  
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS  
; FILE REFERENCE: 010099.03  
; CURRENT APPLICATION NUMBER: US/11/075,185  
; CURRENT FILING DATE: 2005-03-07  
; PRIOR APPLICATION NUMBER: US 60/551,103  
; PRIOR FILING DATE: 2004-03-08  
; PRIOR APPLICATION NUMBER: US 60/568,290  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 78869  
; TYPE: DNA  
; ORGANISM: Sorangium cellulosum  
US-11-075-185-1

Query Match 5.1%; Score 44.2; DB 12; Length 78869;

Best Local Similarity 43.9%; Pred. No. 0.41; Mismatches 243; Indels 0; Gaps 0;

Matches 190; Conservative 0;

Qy 386 GCTTCACCGCTTCCAGCCACCTTATCCGTACCTGACAGACGAGATGACCTGCCACCA 445  
Db 11202 GGGCGCGCGCGGAGAGTGTCTGCTCGCTCCGACGCGCTCGGACGCGCGCTTCGTCCTCA 11261  
Qy 446 CCATCTCGCTGTACAGACGGGAGAGAGCCGCCACCTTACGAGGAGGCGGCTGACCTTCAGC 505  
Db 11262 GCTTCGCAACGAAACCGACGAGGCGCTGCTGCTTCCAGCGCGCTTCGCTGCTCATG 11321  
Qy 506 TTTCGAGACCGGAG 565  
Db 11322 TACGCGGACACCGCTTCGAGTGTCTGCTTCGACGCGGACCGGCGGCGGCGGCTG 11381  
Qy 566 GAACCATCTTTCAGACGTGACGTGATGATGATGATGATGATGATGATGATGATGATGATG 625  
Db 11382 AGCTGCCACCTTACGCTTCGAGCAGAGGCTACTGCTCCAGGCGGCGGAGGCGCTGCGC 11441  
Qy 626 GCAATTAATCTGCGGATGAGCGGACGCTGCTACGCGAGCGGCGGCGGCGGCGGCGGCGG 685  
Db 11442 CCAGCTTCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11501  
Qy 686 CGGCCCACTTACGAGGAGGATGAGGCACTACCGGAGGCTGCTTCCAGCAGCAGCAGCAG 745  
Db 11502 GCTTCGCGGACCGGAGGATGAGTCTTCTACGCGGCGGCTTCTTACAGCAGCAGCAGCAG 11561  
Qy 746 GCAAGTGGCCGCTCTTCTGAGAGGAGCCGGCTCCACCAACACATCGGCC 805  
Db 11562 GGGTCTCGACACACGTGGCTGGGACGCGCTGCTCCGGGACGCGGCTTCGTGAGC 11621  
Qy 806 TAGAGAGCGCAGC 818  
Db 11622 TGGGCTGGGCGGC 11634

## RESULT 12

US-11-052-554A-545/c  
; Sequence 545, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PatentIn version 3.3

SEQ ID NO 545

LENGTH: 2226

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis H37Rv

US-11-052-554A-545

Query Match 5.1%; Score 44; DB 12; Length 2226;

Best Local Similarity 45.6%; Pred. No. 0.35; Mismatches 230; Indels 4; Gaps 1;

Matches 196; Conservative 0;

Qy 313 CCAGAGCGGAGGCTTACGCGCCGCTCGGCGGACCGAGCCGCTGCGGCGGCGGCGGCGGCGG 372  
Db 1208 CCGGTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1149  
Qy 373 GCCAGCGGAGCGCTTCCAGCGGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 432  
Db 1148 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1089  
Qy 433 GACCTCCACCACTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492  
Db 1088 TTATCCCGGAGGATTAAGGACGAGAAATCCGCGCGGCGGCGGCGGCGGCGGCGGCGG 1029  
Qy 493 TGACCCCTTCCAGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 552  
Db 1028 CCAACCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 973  
Qy 553 GCACCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 612  
Db 972 TCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 913  
Qy 613 CCGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 672  
Db 912 GTCTTCCAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 853  
Qy 673 ATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 732  
Db 852 GCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 793  
Qy 733 CAGCAGCAGC 742  
Db 792 CGGCGGCGGCGG 783

## RESULT 13

US-09-925-065A-607564/c

Sequence 607564, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092



;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 607564  
;; LENGTH: 646  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-607564

Query Match 5.0%; Score 43.4; DB 6; Length 646;  
Best Local Similarity 48.6%; Pred. No. 0.44;  
Matches 62; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 79 AAACGCTCTTGTCCAGACGATGAGATCAAGAGCTGAGTTTGTTCAGATCATCATC 138  
DB 529 AAAGCCCTGTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 470  
QY 139 ATCGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 173  
DB 469 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 435

RESULT 14  
US-10-858-730-38  
; Sequence 38, Application US/10858730  
; Publication No. US20050255568A1  
; GENERAL INFORMATION:  
; APPLICANT: Bailey, Richard B.  
; APPLICANT: Blomquist, Paul  
; APPLICANT: Doten, Reed  
; APPLICANT: Driggers, Edward M.  
; APPLICANT: Madden, Kevin T.  
; APPLICANT: O'Leary, Jessica  
; APPLICANT: O'Toole, George  
; APPLICANT: Trueheart, Joshua  
; APPLICANT: Walbridge, Michael J.  
; APPLICANT: Yorgey, Peter S.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID  
; FILE REFERENCE: 14184-030001  
; CURRENT APPLICATION NUMBER: US/10/858,730  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/475,000  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: US 60/551,860  
; PRIOR FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 364  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 2736  
; TYPE: DNA  
; ORGANISM: Streptomyces coelicolor  
US-10-858-730-38

Query Match 5.0%; Score 43.4; DB 8; Length 2736;  
Best Local Similarity 48.6%; Pred. No. 0.49;  
Matches 119; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 273 CCTGTGCGCTTCGAGACAGATGTCAAGCAACGGAATCCCAAGCCCGAGGTCTAAGC 332  
DB 1950 CCGGAGAACTGTGAGCTGACCGTGCAGCACTTCAGGCTTCGCGCAACCGC 2009  
QY 333 CCGGCTTCGAGCCCAAGCCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392  
DB 2010 GCCCGCGCACTTCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2069  
QY 393 CCGCTTCGAGCCCAAGCTTCGTAAGTCAAGCAAGATGCACTTCGCGCGCGCGCG 452  
DB 2190 CCGCTTCGAGCCCAAGCTTCGTAAGTCAAGCAAGATGCACTTCGCGCGCGCGCG 2129

QY 453 GCTGTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 512  
DB 2130 GAGCTTCAGCCCGGTGAGCAAGCTGCGGAGCTGCACTGAGCTGAGCTGAGCTG 2189  
QY 513 CCGCG 517  
DB 2190 CCGCG 2194

RESULT 15  
US-10-750-185-27313/C  
; Sequence 27313, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMT GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27313  
; LENGTH: 7402  
; TYPE: DNA  
; ORGANISM: Bovine 1986680890824  
US-10-750-185-27313

Query Match 5.0%; Score 43.2; DB 8; Length 7402;  
Best Local Similarity 68.2%; Pred. No. 0.59;  
Matches 60; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 100 ATGAGATCAAGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATG 159  
DB 1692 ATAGAGATGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1633  
QY 160 ATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187  
DB 1632 GTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1605

Search completed: February 28, 2006, 10:28:37  
Job time : 1129.53 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:50:15 ; Search time 6670 Seconds  
(without alignments)  
11257.901 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321  
Sequence: 1 cgcacgcgcgtctcgagcga.....ctgcgtagtcgaaagcag 1321

Scoring table: OLIGO-NUC  
Gapop 60.0, Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word-size: 23

Total number of hits satisfying chosen parameters: 8868

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
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5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hlg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	6 AX392417	AX392417 Sequence
2	1302	98.6	4930	6 CS130796	CS130796 Sequence
3	1229	93.0	4839	6 CO812357	CO812357 Sequence
4	1229	93.0	4839	6 CO896247	CO896247 Sequence
5	1229	93.0	4839	6 CO976475	CO976475 Sequence
6	1229	93.0	4839	6 CO981430	CO981430 Sequence
7	1229	93.0	4839	6 AF305616	AF305616 Homo sapi
8	1178	89.2	1383	6 AX775889	AX775889 Sequence
9	909	68.8	4519	6 CO894692	CO894692 Sequence
10	861	65.2	861	6 AX392419	AX392419 Sequence
11	838	63.4	1061	8 BC015918	BC015918 Homo sapi
12	800	60.6	1140	6 AR336830	AR336830 Sequence
13	800	60.6	1141	8 AF224278	AF224278 Homo sapi
14	800	60.6	1818	8 AY128643	AY128643 Homo sapi
15	800	60.6	4531	6 CS130842	CS130842 Sequence
16	800	60.6	4538	6 CS130841	CS130841 Sequence
17	785	57.2	785	6 AR336831	AR336831 Sequence
18	749	56.7	969	6 BD272494	BD272494 Secreted

19	749	56.7	1085	6 AX775887	AX775887 Sequence
20	749	56.7	1913	6 BD272544	BD272544 Secreted
21	744	56.3	969	6 BD272514	BD272514 Secreted
22	704	53.3	759	6 BD272545	BD272545 Secreted
23	701	53.1	753	6 BD272534	BD272534 Secreted
24	701	53.1	756	6 BD272495	BD272495 Secreted
25	698	52.8	969	6 BD272515	BD272515 Secreted
26	698	52.8	969	6 BD272516	BD272516 Secreted
27	647	49.0	1060	8 BC080635	BC080635 Homo sapi
28	600	45.4	600	6 CO728942	CO728942 Sequence
29	593	44.9	61505	8 AF305426	AF305426 Homo sapi
30	593	44.9	130435	8 HS71807	AL035541 Human DNA
31	560	42.4	1583	6 AX593655	AX593655 Sequence
32	521	39.4	150224	8 HSU105917	AL121913 Human DNA
33	401	30.4	408	6 AX071267	AX071267 Sequence
34	302	22.9	693	6 AX392430	AX392430 Sequence
35	271	20.5	812	6 BD226320	BD226320 Pancreati
36	271	20.5	812	6 AX011709	AX011709 Sequence
37	209	15.8	310	6 CO976479	CO976479 Sequence
38	209	15.8	529	6 CO976481	CO976481 Sequence
39	209	15.8	579	6 CO976478	CO976478 Sequence
40	152	11.5	301	6 CO976480	CO976480 Sequence
41	110	8.3	270	6 CO735730	CO735730 Sequence
42	60	4.5	60	6 CO543985	CO543985 Sequence
43	54	4.1	158243	14 CR956367	CR956367 Sus scrofa
44	52	3.9	183457	14 CR956387	CR956387 Sus scrofa
45	51	3.9	51	6 AX199565	AX199565 Sequence
46	44	3.3	411	6 BD272547	BD272547 Secreted
47	44	3.3	484	6 BD272546	BD272546 Secreted
48	44	3.3	484	6 BD272535	BD272535 Secreted
49	44	3.3	651	6 BD272505	BD272505 Secreted
50	44	3.3	651	9 AF220208	AF220208 Mus muscu
51	44	3.3	878	6 AX392428	AX392428 Sequence
52	44	3.3	878	6 BC092094	BC092094 Mus muscu
53	44	3.3	895	9 BC069890	BC069890 Mus muscu
54	44	3.3	1079	9 BC023092	BC023092 Mus muscu
55	44	3.3	1265	5 AJ720618	AJ720618 Gallus ga
56	44	3.3	1379	9 BC036995	BC036995 Mus muscu
57	44	3.3	1713	6 BD272504	BD272504 Secreted
58	44	3.3	1713	6 BD272517	BD272517 Secreted
59	44	3.3	1713	6 BD272518	BD272518 Secreted
60	44	3.3	1713	6 BD272519	BD272519 Secreted
61	44	3.3	156698	9 AL837509	AL837509 Mouse DNA
62	44	3.3	175847	14 AC110189	AC110189 Mus muscu
63	44	3.3	231930	14 AC134911	AC134911 Mus muscu
64	42	3.2	673	6 AX525744	AX525744 Sequence
65	42	3.2	249554	14 AC139417	AC139417 Rattus no
66	42	3.2	258632	14 AC111878	AC111878 Rattus no
67	41	3.1	475	6 AX392431	AX392431 Sequence
68	41	3.1	128625	9 AL837520	AL837520 Mouse DNA
69	37	2.8	179741	14 AC116815	AC116815 Mus muscu
70	34	2.6	640	6 AR617254	AR617254 Sequence
71	34	2.6	2000	6 AX655988	AX655988 Sequence
72	34	2.6	3046	8 HSAJ757	AJ000757 Homo sapi
73	34	2.6	44312	8 AB065453	AB065453 Homo sapi
74	34	2.6	110000	14 AC106698	AC106698 Rattus no
75	34	2.6	110000	14 CT005267	CT005267 of
76	34	2.6	110000	14 CT005267	Continuation (7 of
77	34	2.6	110000	15 AP008205	Continuation (106
78	34	2.6	110000	15 AP008210	Continuation (223
79	34	2.6	112883	8 AC009404	AC009404 Homo sapi
80	34	2.6	118959	15 OSJN00235	AL713159 Oryza sat
81	34	2.6	153308	15 AC118668	AC118668 Genomic s
82	34	2.6	187409	9 AC151572	AC151572 Mus muscu
83	34	2.6	219471	14 AC126463	AC126463 Rattus no
84	34	2.6	219471	14 AC134632	AC134632 Rattus no
85	34	2.6	221100	14 AC112841	AC112841 Rattus no
86	34	2.6	233939	14 AC105853	AC105853 Rattus no
87	34	2.6	237026	14 AC103439	AC103439 Rattus no
88	34	2.6	237151	14 AC137424	AC137424 Rattus no
89	34	2.6	242493	14 AC137322	AC137322 Rattus no
90	34	2.6	247356	14 AC111257	AC111257 Rattus no
91	34	2.6	266344	8 AC005158	AC005158 Homo sapi

92	34	2.6	275229	14	AC098198	AC098198 Rattus no	c 165	32	2.4	258545	14	AC135666	AC135666 Rattus no
93	34	2.6	305075	14	AC106355	AC106355 Rattus no	c 166	32	2.4	259335	14	AC126194	AC126194 Rattus no
C 94	33	2.5	86146	14	AC023805	AC023805 Mus muscu	c 167	32	2.4	279534	14	AC114035	AC114035 Rattus no
C 95	33	2.5	101396	8	AC131182	AC131182 Homo sapi	c 168	32	2.4	281747	14	AC094865	AC094865 Rattus no
C 96	33	2.5	165212	9	AL596125	AL596125 Mouse DNA	c 169	32	2.4	296417	14	AC112730	AC112730 Rattus no
C 97	33	2.5	172172	14	AC069030	AC069030 Homo sapi	c 170	32	2.4	303425	14	AC111410	AC111410 Rattus no
98	33	2.5	229482	14	AC074149	AC074149 Mus muscu	c 171	31	2.3	359	6	AR617715	AR617715 Sequence
99	32	2.4	274	10	BV102379	BV102379 RPMSB00	c 172	31	2.3	357	10	BV105358	BV105358 MARC 5563
100	32	2.4	577	6	CQ057943	CQ057943 Sequence	c 173	31	2.3	533	6	AR617857	AR617857 Sequence
101	32	2.4	577	6	CQ077251	CQ077251 Sequence	c 174	31	2.3	645	6	CQ609324	CQ609324 Sequence
102	32	2.4	577	6	CQ108252	CQ108252 Sequence	c 175	31	2.3	834	15	AK105087	AK105087 Oryza sat
103	32	2.4	577	6	CQ146881	CQ146881 Sequence	c 176	31	2.3	915	15	AK120273	AK120273 Oryza sat
104	32	2.4	577	6	CQ182292	CQ182292 Sequence	c 177	31	2.3	936	15	AK072488	AK072488 Oryza sat
105	32	2.4	577	6	CQ206688	CQ206688 Sequence	c 178	31	2.3	2332	6	AX747175	AX747175 Sequence
106	32	2.4	577	6	CQ230106	CQ230106 Sequence	c 179	31	2.3	2332	6	AK081771	AK081771 Sequence
107	32	2.4	577	6	CQ268254	CQ268254 Sequence	c 180	31	2.3	2808	6	CQ609323	CQ609323 Sequence
108	32	2.4	577	6	CQ305288	CQ305288 Sequence	c 181	31	2.3	28202	14	AC017459	AC017459 Drosophill
109	32	2.4	577	6	CQ342489	CQ342489 Sequence	c 182	31	2.3	59078	8	AL606807	AL606807 Human DNA
110	32	2.4	834	15	AK062882	AK062882 Oryza sat	c 183	31	2.3	67987	9	AL672157	AL672157 Mouse DNA
111	32	2.4	1804	9	BC026781	BC026781 Mus muscu	c 184	31	2.3	70811	14	AC117542	AC117542 Mus muscu
112	32	2.4	1810	9	BC058223	BC058223 Mus muscu	c 185	31	2.3	100580	8	BS000235	BS000235 Pan trogl
113	32	2.4	1964	6	CQ052940	CQ052940 Sequence	c 186	31	2.3	110000	15	BX572642_4	Continuation (5 of
114	32	2.4	1964	6	CQ068034	CQ068034 Sequence	c 187	31	2.3	110000	15	AP008215_043	Continuation (44 o
115	32	2.4	1964	6	CQ095094	CQ095094 Sequence	c 188	31	2.3	110000	15	AP008207_025	Continuation (26 o
116	32	2.4	1964	6	CQ133842	CQ133842 Sequence	c 189	31	2.3	110000	15	AP008213_294	Continuation (295
117	32	2.4	1964	6	CQ172380	CQ172380 Sequence	c 190	31	2.3	114288	8	AP000590	AP000590 Homo sapi
118	32	2.4	1964	6	CQ201552	CQ201552 Sequence	c 191	31	2.3	115150	14	AP005736	AP005736 Oryza sat
119	32	2.4	1964	6	CQ217078	CQ217078 Sequence	c 192	31	2.3	134793	15	AP006441	AP006441 Oryza sat
120	32	2.4	1964	6	CQ255656	CQ255656 Sequence	c 193	31	2.3	147274	14	AP005588	AP005588 Oryza sat
121	32	2.4	1964	6	CQ292752	CQ292752 Sequence	c 194	31	2.3	149773	14	AC118209	AC118209 Mus muscu
122	32	2.4	1964	6	CQ292738	CQ292738 Sequence	c 195	31	2.3	151263	15	AP004333	AP004333 Oryza sat
C 123	32	2.4	2000	6	AX656401	AX656401 Sequence	c 196	31	2.3	157112	15	AP002872	AP002872 Oryza sat
C 124	32	2.4	2717	9	AB045590	AB045590 Rattus no	c 197	31	2.3	159524	14	AC155302	AC155302 Mus muscu
C 125	32	2.4	2825	15	AK120262	AK120262 Oryza sat	c 198	31	2.3	160033	8	BS000236	BS000236 Pan trogl
C 126	32	2.4	2916	13	CHKCMOPLF	CHKCMOPLF Chicken mRN	c 199	31	2.3	167029	15	AP002540	AP002540 Oryza sat
C 127	32	2.4	3171	13	AAFWAF	AAFWAF Avian galli	c 200	31	2.3	170510	15	AP005589	AP005589 Oryza sat
C 128	32	2.4	3960	5	CHKCMF	D25596 Gallus galli	c 201	31	2.3	174375	14	AC128360	AC128360 Rattus no
C 129	32	2.4	56475	8	AL353658	AL353658 Human DNA	c 202	31	2.3	174520	14	BS000234	BS000234 Pan trogl
C 130	32	2.4	73803	15	NCB11B22	AL356834 Neurospor	c 203	31	2.3	174520	14	AC157456	AC157456 Oryctoleg
C 131	32	2.4	95637	15	BX842594	BX842594 Neurospor	c 204	31	2.3	180048	8	AC157456	AC160121 Mus muscu
C 132	32	2.4	110000	14	AC109084_1	Continuation (2 of	c 205	31	2.3	181751	14	AC160121	AC092487 Homo sapi
C 133	32	2.4	110000	15	AP008214_233	Continuation (234	c 206	31	2.3	183301	14	AC092487	AC092487 Drosophill
C 134	32	2.4	110000	15	AP008207_279	Continuation (280	c 207	31	2.3	188489	2	AC012098	AC146153 Pan trogl
C 135	32	2.4	111388	8	AC016655	AC016655 Homo sapi	c 208	31	2.3	188640	14	AC146153	AC010708 Drosophill
C 136	32	2.4	115487	14	AC027344	AC027344 Homo sapi	c 209	31	2.3	188766	2	AC010708	AC079023 Mus muscu
C 137	32	2.4	124752	8	AC010419	AC010419 Homo sapi	c 210	31	2.3	189982	14	AC079023	AC152976 Mus muscu
C 138	32	2.4	142182	15	AP004399	AP004399 Oryza sat	c 211	31	2.3	194151	9	AC152976	AC006028 Homo sapi
C 139	32	2.4	153223	14	AC018548	AC018548 Homo sapi	c 212	31	2.3	210608	8	AC006028	AC133836 Rattus no
C 140	32	2.4	159324	8	AC146165	AC146165 Pan trogl	c 213	31	2.3	224817	14	AC133836	AC11840 Rattus no
C 141	32	2.4	160945	14	AC149910	AC149910 Strongylo	c 214	31	2.3	232183	14	AC11840	AC116962 Oryctoleg
C 142	32	2.4	160956	14	AC013637	AC013637 Homo sapi	c 215	31	2.3	232368	14	AC116962	AC110445 Rattus no
C 143	32	2.4	161462	14	AC136669	AC136669 Rattus no	c 216	31	2.3	242299	14	AC110445	AC110445 Rattus no
C 144	32	2.4	172525	8	AC008514	AC008514 Homo sapi	c 217	31	2.3	247269	9	AC120819	AC120819 Rattus no
C 145	32	2.4	173837	8	AC124681	AC124681 Mus muscu	c 218	31	2.3	257790	14	AC15767	AC115767 Mus muscu
C 146	32	2.4	179372	14	AC040922	AC040922 Homo sapi	c 219	31	2.3	261710	14	AC107431	AC107431 Rattus no
C 147	32	2.4	179978	9	AC134561	AC134561 Mus muscu	c 220	31	2.3	276741	14	AC096301	AC096301 Rattus no
C 148	32	2.4	184123	14	AC163215	AC163215 Mus muscu	c 221	31	2.3	297155	14	AC095921	AC095921 Rattus no
C 149	32	2.4	190025	14	AC140145	AC140145 Homo sapi	c 222	31	2.3	315109	2	AB003509	AB003509 Oryza sat
C 150	32	2.4	190149	14	AC122097	AC122097 Rattus no	c 223	30	2.3	1922	15	AK100086	BC021906 Homo sapi
C 151	32	2.4	192183	14	AC134492	AC134492 Rattus no	c 224	30	2.3	2383	8	BC021906	AC11605 Emiliania
C 152	32	2.4	194459	15	AP003335	AP003335 Oryza sat	c 225	30	2.3	35119	14	AC151605	AC105344 Homo sapi
C 153	32	2.4	198582	8	AC005291	AC005291 Homo sapi	c 226	30	2.3	35713	8	AC105344	AC105344 Homo sapi
C 154	32	2.4	202301	9	AC157950	AC157950 Mus muscu	c 227	30	2.3	70881	8	BX284660	BX284660 Human DNA
C 155	32	2.4	202525	9	AC157950	AC157950 Mus muscu	c 228	30	2.3	79591	8	HSJ908M4	HSJ908M4 Human DNA
C 156	32	2.4	204257	9	AC138676	AC138676 Mus muscu	c 229	30	2.3	99497	8	HS29316	AL049749 Human DNA
C 157	32	2.4	215695	9	AC148095	AC148095 Mus muscu	c 230	30	2.3	100974	14	AC104715	AC104715 Oryza sat
C 158	32	2.4	221080	14	AC106160	AC106160 Rattus no	c 231	30	2.3	110000	14	AC091352_1	Continuation (3 of
C 159	32	2.4	222814	9	AC134591	AC134591 Mus muscu	c 232	30	2.3	110000	14	AC091352_2	Continuation (6 of
C 160	32	2.4	226791	14	AC094199	AC094199 Rattus no	c 233	30	2.3	110000	14	AC091371_05	Continuation (7 of
C 161	32	2.4	239018	14	AC106602	AC106602 Rattus no	c 234	30	2.3	110000	15	AP008214_041	Continuation (42 o
C 162	32	2.4	242543	14	AC096128	AC096128 Rattus no	c 235	30	2.3	110000	15	AP008209_270	Continuation (271
C 163	32	2.4	247458	14	AC164607	AC164607 Mus muscu	c 236	30	2.3	110000	15	AP008211_255	Continuation (256
C 164	32	2.4	249600	14	AC126988	AC126988 Rattus no	c 237	30	2.3	110000	15	AP008211_255	Continuation (256

C 238	30	2.3	111882	15	AC087851	AC087851 Oryza sat	311	2.2	446	6	C0058092	C0058092 Sequence
C 239	30	2.3	120627	14	AC104714	AC104714 Oryza sat	312	2.2	446	6	C0077409	C0077409 Sequence
C 240	30	2.3	136989	9	AC116710	AC116710 Mus muscu	29	2.2	446	6	C0108423	C0108423 Sequence
C 241	30	2.3	142215	8	AC133065	AC133065 Homo sapi	29	2.2	446	6	C0147064	C0147064 Sequence
C 242	30	2.3	148205	15	AP005606	AP005606 Oryza sat	29	2.2	446	6	C0182449	C0182449 Sequence
C 243	30	2.3	161701	14	AC117110	AC117110 Rattus no	29	2.2	446	6	C0206851	C0206851 Sequence
C 244	30	2.3	166406	9	AC124005	AC124005 Mus muscu	29	2.2	446	6	C0230291	C0230291 Sequence
C 245	30	2.3	169073	15	AC132491	AC132491 Oryza sat	29	2.2	446	6	C0268426	C0268426 Sequence
C 246	30	2.3	169585	14	AC078821	AC078821 Homo sapi	29	2.2	446	6	C0305460	C0305460 Sequence
C 247	30	2.3	174776	14	AC163265	AC163265 Rhinolph	29	2.2	446	6	C0342654	C0342654 Sequence
C 248	30	2.3	178807	14	AC166597	AC166597 Nomauscu	29	2.2	614	10	BV379979	BV379979 Sequence
C 249	30	2.3	179394	8	AC010619	AC010619 Homo sapi	29	2.2	631	10	HSNCAD1X	HSNCAD1X Sequence
C 250	30	2.3	180585	14	AC131828	AC131828 Rattus no	29	2.2	646	10	BV018795	BV018795 Sequence
C 251	30	2.3	184908	9	AC102278	AC102278 Mus muscu	29	2.2	748	6	C0412532	C0412532 Sequence
C 252	30	2.3	185723	9	AC115316	AC115316 Rattus no	29	2.2	913	2	AY542994	AY542994 Sequence
C 253	30	2.3	194013	9	AL591905	AL591905 Mouse DNA	29	2.2	1012	8	AY358811	AY358811 Sequence
C 254	30	2.3	209245	14	AC151894	AC151894 Aotus nan	29	2.2	1094	9	AF075291	AF075291 Sequence
C 255	30	2.3	209844	8	AC011495	AC011495 Homo sapi	29	2.2	1128	6	BC006245	BC006245 Sequence
C 256	30	2.3	211094	14	AC133625	AC133625 Rattus no	29	2.2	1466	6	C0899377	C0899377 Sequence
C 257	30	2.3	214493	14	AC097047	AC097047 Rattus no	29	2.2	1546	6	CS008054	CS008054 Sequence
C 258	30	2.3	217342	14	AC119700	AC119700 Rattus no	29	2.2	1546	6	AX928527	AX928527 Sequence
C 259	30	2.3	220179	14	AC115232	AC115232 Rattus no	29	2.2	1546	6	AX951780	AX951780 Sequence
C 260	30	2.3	223642	14	AC108290	AC108290 Rattus no	29	2.2	1546	6	AX960058	AX960058 Sequence
C 261	30	2.3	225465	14	AC126882	AC126882 Rattus no	29	2.2	1546	6	AF075292	AF075292 Sequence
C 262	30	2.3	227369	14	AC114469	AC114469 Rattus no	29	2.2	1570	6	BD234761	BD234761 Sequence
C 263	30	2.3	228381	14	AC103262	AC103262 Rattus no	29	2.2	1656	6	AX659956	AX659956 Sequence
C 264	30	2.3	230077	14	AC099450	AC099450 Rattus no	29	2.2	1710	9	BC003901	BC003901 Sequence
C 265	30	2.3	232900	14	AC103264	AC103264 Rattus no	29	2.2	2138	8	AK096881	AK096881 Sequence
C 266	30	2.3	233976	14	AC118078	AC118078 Rattus no	29	2.2	2506	8	BC096440	BC096440 Sequence
C 267	30	2.3	237078	14	AC098669	AC098669 Rattus no	29	2.2	2608	6	AX658366	AX658366 Sequence
C 268	30	2.3	237078	14	AC110347	AC110347 Rattus no	29	2.2	2627	15	AK103005	AK103005 Sequence
C 269	30	2.3	239600	9	AC097420	AC097420 Rattus no	29	2.2	2654	15	AK106611	AK106611 Sequence
C 270	30	2.3	239600	9	AC139128	AC139128 Mus muscu	29	2.2	2853	8	HSNCAD	HSNCAD Sequence
C 271	30	2.3	239932	14	AC095276	AC095276 Rattus no	29	2.2	2913	9	AF109773	AF109773 Sequence
C 272	30	2.3	240336	14	AC094844	AC094844 Rattus no	29	2.2	2987	8	BC006190	BC006190 Sequence
C 273	30	2.3	240510	14	AC134371	AC134371 Rattus no	29	2.2	3266	6	C0413290	C0413290 Sequence
C 274	30	2.3	246875	14	AC130059	AC130059 Rattus no	29	2.2	3431	6	C0717870	C0717870 Sequence
C 275	30	2.3	247664	14	AC125774	AC125774 Rattus no	29	2.2	3444	8	AF028706	AF028706 Sequence
C 276	30	2.3	247766	14	AC119322	AC119322 Rattus no	29	2.2	3681	8	AF152658	AF152658 Sequence
C 277	30	2.3	248294	14	AC113969	AC113969 Rattus no	29	2.2	4122	8	BC036470	BC036470 Sequence
C 278	30	2.3	248367	14	AC094853	AC094853 Rattus no	29	2.2	4133	6	C0824160	C0824160 Sequence
C 279	30	2.3	251003	14	AC131000	AC131000 Rattus no	29	2.2	5370	6	C0581298	C0581298 Sequence
C 280	30	2.3	251790	14	AC099003	AC099003 Rattus no	29	2.2	5464	2	AY051657	AY051657 Sequence
C 281	30	2.3	254460	14	AC132183	AC132183 Rattus no	29	2.2	5552	2	DROPLC21A	DROPLC21A Sequence
C 282	30	2.3	254650	14	AC128790	AC128790 Rattus no	29	2.2	5719	9	AF327569	AF327569 Sequence
C 283	30	2.3	256398	14	AC130952	AC130952 Rattus no	29	2.2	5750	6	C0581297	C0581297 Sequence
C 284	30	2.3	257028	14	AC112276	AC112276 Rattus no	29	2.2	44868	14	AC017345	AC017345 Sequence
C 285	30	2.3	263297	14	AC127631	AC127631 Rattus no	29	2.2	37996	6	CS081297	CS081297 Sequence
C 286	30	2.3	265566	14	AC123187	AC123187 Rattus no	29	2.2	67995	14	AC100485	AC100485 Sequence
C 287	30	2.3	269740	14	AC133056	AC133056 Rattus no	29	2.2	80101	2	AC004115	AC004115 Sequence
C 288	30	2.3	271437	14	AC132564	AC132564 Rattus no	29	2.2	81010	8	AC087245	AC087245 Sequence
C 289	30	2.3	274467	14	AC113707	AC113707 Rattus no	29	2.2	93342	8	HS137415	HS137415 Sequence
C 290	30	2.3	274766	14	AC135283	AC135283 Rattus no	29	2.2	109339	15	AP008215	AP008215 Sequence
C 291	30	2.3	284834	14	AC135643	AC135643 Rattus no	29	2.2	110000	15	AP008215_035	AP008215_035 Sequence
C 292	30	2.3	286789	14	AC133723	AC133723 Rattus no	29	2.2	110000	15	AP008215_028	AP008215_028 Sequence
C 293	30	2.3	287586	14	AC103294	AC103294 Rattus no	29	2.2	119077	14	AC147494	AC147494 Sequence
C 294	30	2.3	291270	14	AC103294	AC103294 Rattus no	29	2.2	119116	14	AC152131	AC152131 Sequence
C 295	30	2.3	293834	14	AC135528	AC135528 Rattus no	29	2.2	130569	8	CNS08888	CNS08888 Sequence
C 296	30	2.3	349528	14	AC096643	AC096643 Rattus no	29	2.2	131691	8	CNS08888	CNS08888 Sequence
C 297	29	2.2	227	15	AY023293	AY023293 Oryza sat	29	2.2	140620	15	AP008207_370	AP008207_370 Sequence
C 298	29	2.2	230	15	AY022724	AY022724 Oryza sat	29	2.2	110000	15	AP008209_173	AP008209_173 Sequence
C 299	29	2.2	233	15	AY022902	AY022902 Oryza sat	29	2.2	110000	15	AP008210_057	AP008210_057 Sequence
C 300	29	2.2	383	15	AY0308814	AY0308814 Canis fam	29	2.2	110000	15	AP008211_058	AP008211_058 Sequence
C 301	29	2.2	401	6	C0053092	C0053092 Sequence	29	2.2	119116	14	AC147494	AC147494 Sequence
C 302	29	2.2	401	6	C0068196	C0068196 Sequence	29	2.2	119116	14	AC152131	AC152131 Sequence
C 303	29	2.2	401	6	C0095270	C0095270 Sequence	29	2.2	130569	8	CNS08888	CNS08888 Sequence
C 304	29	2.2	401	6	C0134027	C0134027 Sequence	29	2.2	130569	8	CNS08888	CNS08888 Sequence
C 305	29	2.2	401	6	C0172540	C0172540 Sequence	29	2.2	131691	8	CNS08888	CNS08888 Sequence
C 306	29	2.2	401	6	C0201717	C0201717 Sequence	29	2.2	131691	8	CNS08888	CNS08888 Sequence
C 307	29	2.2	401	6	C0217267	C0217267 Sequence	29	2.2	137422	15	AC135598	AC135598 Sequence
C 308	29	2.2	401	6	C0255831	C0255831 Sequence	29	2.2	140620	15	CNS08888	CNS08888 Sequence
C 309	29	2.2	401	6	C0292927	C0292927 Sequence	29	2.2	140620	15	AP003415	AP003415 Sequence
C 310	29	2.2	401	6	C0329907	C0329907 Sequence	29	2.2	145456	8	AL513366	AL513366 Sequence

C 384	2.2	146728	15	AP005396
C 385	2.2	146954	15	AP004635
C 386	2.2	151721	15	AP003943
C 387	2.2	152075	14	CNS07EPL
C 388	2.2	152090	14	CNS08C82
C 389	2.2	152406	14	AP005711
C 390	2.2	153388	15	AP003289
C 391	2.2	154378	15	AP001383
C 392	2.2	157981	15	AP006170
C 393	2.2	160135	14	BX649519
C 394	2.2	160894	14	AC135433
C 395	2.2	162946	8	AL772409
C 396	2.2	163946	8	AC146411
C 397	2.2	163461	2	AC008371
C 398	2.2	166677	2	AC115482
C 399	2.2	166745	8	AC096718
C 400	2.2	175154	8	AC093246
C 401	2.2	178882	14	AC158270
C 402	2.2	180355	15	AP005504
C 403	2.2	180673	9	AC068627
C 404	2.2	188010	14	AC134264
C 405	2.2	188908	9	AC110034
C 406	2.2	191110	14	AC121413
C 407	2.2	197082	8	AC006249
C 408	2.2	197714	14	AC128967
C 409	2.2	200491	8	AC007249
C 410	2.2	201430	14	HS7706
C 411	2.2	202825	14	AC161926
C 412	2.2	204136	9	AL772271
C 413	2.2	204407	14	AC021446
C 414	2.2	208848	14	AC139608
C 415	2.2	211795	14	AC125690
C 416	2.2	217838	14	AC132673
C 417	2.2	217867	14	AC095149
C 418	2.2	220480	14	AC023973
C 419	2.2	221776	14	AC136253
C 420	2.2	227533	14	AC094895
C 421	2.2	227605	14	AC121445
C 422	2.2	231930	14	AC134911
C 423	2.2	234137	8	AC157525
C 424	2.2	236966	9	AC126408
C 425	2.2	236969	14	AC113710
C 426	2.2	239069	14	AC108289
C 427	2.2	239591	14	AC128432
C 428	2.2	239945	14	AC094050
C 429	2.2	242130	14	AC108556
C 430	2.2	243151	14	CR956424
C 431	2.2	245174	14	AC095157
C 432	2.2	245582	9	AC140073
C 433	2.2	248254	14	AC133448
C 434	2.2	250175	14	AC160494
C 435	2.2	250188	14	AC110100
C 436	2.2	250207	14	AC096136
C 437	2.2	251158	14	AC117023
C 438	2.2	252115	14	AC131854
C 439	2.2	257028	14	AC112276
C 440	2.2	259747	14	AL136447
C 441	2.2	260041	14	AC153186
C 442	2.2	260041	14	AC153186
C 443	2.2	269117	14	AC115400
C 444	2.2	269155	9	AC109138
C 445	2.2	271135	14	AC105492
C 446	2.2	306076	2	AE003589
C 447	2.1	216	8	HDMHUNTPEA
C 448	2.1	224	15	AY023274
C 449	2.1	305	8	HDMEMELA
C 450	2.1	321	6	AX05271
C 451	2.1	360	15	AY526437
C 452	2.1	401	10	BV192862
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AC110034	Mus muscu
AC121413	Rattus no
AC006249	Homo sapi
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AC007249	Homo sapi
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AC108289	Rattus no
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AC140073	Mus muscu
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LOCUS	AX392417				
DEFINITION	Sequence 1 from Patent WO0216416.				
ACCESSION	AX392417				
VERSION	AX392417.1	GI:19700732			
KEYWORDS					
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ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1				
AUTHORS	Lee, R.T., Landeschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.				
TITLE	Diagnosis and treatment of cardiovascular conditions				
JOURNAL	Patent: WO 0216416-A 1 28-FEB-2002;				
FEATRES	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)				
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Query Match 100.0%; Score 1321; DB 6; Length 1321;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION CS130796  
 VERSION CS130796.1 GI:71792866  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 Homnidae; Homo.  
 REFERENCE 1  
 OEBTOLF, T.F.  
 AUTHORS OEBTOLF, T.F.  
 TITLE Classification of cancer  
 JOURNAL Patent: WO 2005064009-A 82 14-JUN-2005;  
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Query Match 98.6%; Score 1302; DB 6; Length 4930;  
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 Matches 1302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 109 from Patent WO2004038020.
ACCESSION CQ812357
VERSION CQ812357.1 GI:47601977
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
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Waltig,R., Pousetka,A., Mollenhauer,J. and Schendendorf,D.
Target genes for the diagnosis and treatment of cancer
Patent: WO 2004038020-A 109 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)

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Query Match 93.0%; Score 1229; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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 LOCUS CQ896247 Sequence 71 from Patent WO2004076614.  
 DEFINITION CQ896247  
 ACCESSION CQ896247.1 GI:55468096  
 VERSION CQ896247.1  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE  
 1. Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A.,  
 Beekmann, G., Brumentendorf, T., Kimmernann, H., Roepcke, S., Hermann, K.,  
 Kitzhong, L., Pillarsky, C. and Staub, E.  
 Human nucleic acid sequences obtained from prostatic carcinomas  
 Patent: WO 2004076614-A 71 10-SEP-2004;  
 Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);  
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 Location/Qualifiers  
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Query Match 93.0%; Score 1229; DB 6; Length 4839;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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 QY 213 GGGGCGAGCGAGCGGCTCCCGGCACTGAGCCCGGCGGCGCCCGGAACTTGGCGGC 272  
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 QY 573 TGTGTGTGTGATCACTGCTGCTGAGCCACTCAAGACTGTCTGACAGGCTCTTCATCA 632  
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 QY 633 GCCGCGACAGCGGAGGCGAGAGAGAAATGCTCTGTCTCTCAGAGATGCTGTGGC 692  
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DEFINITION Sequence 166 from Patent WO2004113571.  
ACCESSION CQ976475  
VERSION CQ976475.1 GI:57975803  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Einstein, R., McGowan, K.M. and Pando, M.P.  
JOURNAL Prostate specific genes and the use thereof as targets for prostate  
cancer therapy and diagnosis  
Patent: WO 2004113571-A 166-29-DEC-2004;  
Exonhit Therapeutics S.A. (FR)  
FEATURES  
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DB 61 TTCGCGAGCGGCGCGGCGGCGCACTGCGAGCGCGCGCGGCGCTGCGAGGAGGCGCGG 120  
QY 213 GGGCGCAGCGAGCGCGGTCCCGCGCACTGAGCGCGCGCGCGCGGAACTTGGCGG 272  
DB 121 GGGCGCAGCGAGCGCGGTCCCGCGCACTGAGCGCGCGCGCGCGGAACTTGGCGG 180  
QY 273 GACCCGAGCGCGGCGAGCGCGGCGCTCCCGCGCGCGCGCTTCTGCAATGCGGAGC 332  
DB 181 GACCCGAGCGCGGCGAGCGCGGCGCGCTCCCGCGCGCGCGCTTCTGCAATGCGGAGC 240  
QY 333 CCCAGCTCCGCGGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 392  
DB 241 CCCAGCTCCGCGGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 300  
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DB 541 GCGCGCAACAGCGAGGCGGAGAGAGATGCGCTGTCCTAGAGAGATGCTGTGAGC 600  
QY 693 CTTGAGAGAGACAGATGTCAGAGCAACCGAAATCCAGAGCGCGAGTCTAGCGCCGCTC 752  
DB 601 CTTGAGAGAGACAGATGTCAGAGCAACCGAAATCCAGAGCGCGAGTCTAGCGCCGCTC 660  
QY 753 GGGCCACCGACCGCTGCGCGGCGGCTTCCGCGGAGCGGAGCGCTTCAACGCTTCC 812  
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RESULT 6  
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DEFINITION Sequence 285 from Patent EP1498424.  
ACCESSION CQ981430  
VERSION CQ981430.1 GI:58190720  
KEYWORDS  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1  
 AUTHORS Rosenthal, A., Hermann, K., Heiden, E., Pilarsky, C., Brummendorf, T.,  
 Staub, E., Roepcke, S., Wennerich, D., Kimmernann, H. and Li, X.  
 TITLE Human nucleic acid sequences from lung tumours  
 JOURNAL Patent: EP 1498424-A 285 19-JAN-2005;  
 Hitzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE);  
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 ACCESSION AF305616  
 VERSION AF305616.1 GI:16303741  
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 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 4839)  
 AUTHORS Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.  
 TITLE Characterization of a novel gene, STAG1/PMEP1, upregulated in  
 renal cell carcinoma and other solid tumors  
 JOURNAL Mol. Carcinog. 32 (1), 44-53 (2001)  
 PUBMED 11568975  
 REFERENCE 2 (bases 1 to 4839)  
 AUTHORS Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.  
 TITLE Direct Submission  
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 Queensland University of Technology, 2 George St, Brisbane, QLD  
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 DEFINITION Sequence 2 from Patent EP1471075.  
 ACCESSION CO894692  
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Klausner, R. D., Collins, F. S., Wagner, R. L., Sherman, C. M., Schuller, G. D., Altschul, S. F., Zeeberg, B., Bietow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Datchenkov, L., Marinina, K., Farmer, A. A., Rudin, G. N., Hong, L., Stetleiron, M., Soares, M. B., Bonaldo, M. F., Casavari, E. L., Schneer, T. E., Brownstein, M. J., Udén, T. B., Toshiyuki, S., Caminchi, P., Raha, S. S., Loquebiano, N. A., Peters, G. J., Pirange, C.









LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
LOCUS AY128643	1818 bp mRNA linear	AY128643	1	GI:22121998		Homo sapiens (human)	Brunschwig, E.B., Wilson, K., Mack, D., Dawson, D., Lawrence, E., Willis, J.K., Lu, S., Nozari, A., Rello, R.M., Swinler, S., Beard, L., Lutterbaugh, J.D., Willis, J., Platzer, P. and Markowitz, S.	PMEP1, a transforming growth factor-beta-induced marker of	
100	CGAGACTGGAATTGTTTCAGATCATCATCTGCTGCTGATATGATGATGATGATG	159							
582	TGATCAGCTGCTCTGTGAGCCACTAACAGCTGTGTGACCGGTCTTATCATCGCGGAC	641							
160	TGATCAGGTGCTGTCTGTGAGCAGTAAAGAGTGTGTGACCGGTCTTATCATCGCGGAC	219							
642	GCCAGGGGCGGAGAGAGAAATATGCTGTCTTCAAGAAAGATGCTGTGTGCTTGTGAGA	701							
220	GCCAGGGGCGGAGAGAGAAATATGCTGTCTTCAAGAAAGATGCTGTGTGCTTGTGAGA	279							
702	GCAAGTGTCAAGGCAAGGAATCCAGAGCGCGAGGTCTAAGCGCCCGCTCGGCCACCG	761							
280	GCAAGTGTCAAGGCAAGGAATCCAGAGCGCGAGGTCTAAGCGCCCGCTCGGCCACCG	339							
762	ACCGCTGTGCGCGCTGTGCGCCAGCGGAGCGGCTTCCACGCTTCCAGCCCACT	821							
340	ACCGCTGTGCGCGCTGTGCGCCAGCGGAGCGGCTTCCACGCTTCCAGCCCACT	399							
822	ATCGGTACTGTGAGACGAGATTCGACTTGTCCACCTCATCTTGTGTCAAGCGGGAGG	881							
400	ATCGGTACTGTGAGACGAGATTCGACTTGTCCACCTCATCTTGTGTCAAGCGGGAGG	459							
882	AGCCCCACCTTACCGAGGGCCCTGTGACCTTCAGCTTGGGAGCCCGAGAGAGCTGG	941							
460	AGCCCCACCTTACCGAGGGCCCTGTGACCTTCAGCTTGGGAGCCCGAGAGAGCTGG	519							
942	AACTGAACCGGGAGTCTGCTGTGCGCGACCCCAACAGAACCATCTTTCAGAGTGA	1001							
520	AACTGAACCGGGAGTCTGCTGTGCGCGACCCCAACAGAACCATCTTTCAGAGTGA	579							
1002	TGATATGTGCGAGCTGTGCGCGCGCCCTGTGCGCCCGAGAGTACTTGTGCGGAT	1061							
580	TGATATGTGCGAGCTGTGCGCGCGCCCTGTGCGCCCGAGAGTACTTGTGCGGAT	639							
1062	CTGTGTTACGGCAGCGCGCGGGGCGCATATGAGGGGGCGCGCCCACTTACAGCGAGCTAT	1121							
640	CTGTGTTACGGCAGCGCGCGGGGCGCATATGAGGGGGCGCGCCCACTTACAGCGAGCTAT	699							
1122	GCCACTTACCGCGGGGTCTCTCTTCCAGACACAGCAGAGAGTGTGGCGCGCTCTTGTCT	1181							
700	GCCACTTACCGCGGGGTCTCTCTTCCAGACACAGCAGAGAGTGTGGCGCGCTCTTGTCT	759							
1182	AGGGGACCGCGCTTCCACCAACACACATCGCGCCCTTATGAGAGCGCAGCCATCTGAGCA	1241							
760	AGGGGACCGCGCTTCCACCAACACACATCGCGCCCTTATGAGAGCGCAGCCATCTGAGCA	819							
1242	AAAGAGAGGATTAACGAAAGAGACCTCTTATGAGGTCCCAAGGGGGGCGGGGTGGGG	1301							
820	AAAGAGAGGATTAACGAAAGAGACCTCTTATGAGGTCCCAAGGGGGGCGGGGTGGGG	879							
1302	CTGGGTAGGTGAAAAGGCGAG	1321							
880	CTGGGTAGGTGAAAAGGCGAG	899							

	JOURNAL	terminal colonocyte differentiation whose expression is maintained in primary and metastatic colon cancer
	PUBMED	Cancer Res. 63 (7), 1568-1575 (2003)
	12670906	
	TITLE	2 (bases 1 to 1818)
	AUTHORS	Brunschwig,F.B., Willson,K., Mack,D., Dawson,D., Lawrence,E., Willson,J.K.V., Lu,S., Noorati,A., Swisher,S., Beard,L., Luttrebaugh,J.D., Willis,J., Plutzer,P. and Markowitz,S.
	JOURNAL	Direct Submission
	REFERENCE	Submitted (03-JUL-2002) Department of Medicine, Case Western Reserve University/Howard Hughes Medical Institute, 11001 Cedar Ave., Cleveland, OH 44106, USA
	FEATURES	Location/Qualifiers
	SOURCE	1..1818
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		/protein_id="AA089277.1"
		/db_xref="GI:22121999"
		/translation="MMVMVVITCLISHYKLARSFISRHSQGRREDRLASEGLWME SESVSGNGCIPEPVYVAPRPRTDRLAPRAQRPRRPOPTYLOHEIDLPTSLI SDGEPPPYGQPCPLLQLRDPEQLELRKESVRAPNNTIPDSLDMSARLGGPPRSS NSGISATVCGSGMGEGPPTPSIVIGHYPSSFOHOSSGPSPLLBGTIRLHTTHIAE LESNAIWSKEKDQKGHPD"
ORIGIN		
Query Match	60.6%; Score 800; DB 8; Length 1818;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 800; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	522 CGAGCTGGAGATTGTTCAAGTACATCATCAGTCGTGATGATGGTGAATGGTGATGG	581
DB	104 CGAGCTGGAGATTGTTCAAGTACATCATCAGTCGTGATGATGGTGAATGGTGATGG	163
QY	582 TGATCAGTGCCTGCTGAGCCACTACAAGCTGTGTGACGGTCCCTTCATCAGCGGGACA	641
DB	164 TGATCAGTGCCTGCTGAGCCACTACAAGCTGTGTGACGGTCCCTTCATCAGCGGGACA	223
QY	642 GCCAGGGCGGAGAGAGAAGATGCCCTGTCTTCAAGAAATGCTCTTGAGGCTCTCGGAGA	701
DB	224 GCCAGGGCGGAGAGAGAAGATGCCCTGTCTTCAAGAAATGCTCTTGAGGCTCTCGGAGA	283
QY	702 GCACAGTGTACGGCAAGGAATCCACAGGCGGAGGTCTACGCCCGGCTCGGCCACCG	761
DB	284 GCACAGTGTACGGCAAGGAATCCACAGGCGGAGGTCTACGCCCGGCTCGGCCACCG	343
QY	762 ACCGCTTGCCGCTGCGCTTTCGCCACGCGGGAGCGCTTCACCGCTTCAGGCCACT	821
DB	344 ACCGCTTGCCGCTGCGCTTTCGCCACGCGGGAGCGCTTCACCGCTTCAGGCCACT	403
QY	822 ATCCGTACTGACAGCACGATTCGACTTGCACCACATCTTCGTGTTCACACGGGAGAG	881
DB	404 ATCCGTACTGACAGCACGATTCGACTTGCACCACATCTTCGTGTTCACACGGGAGAG	463
QY	882 AGCCCCACCTTACACAGGAGCCCTTCGACCTTCAGCTTCGGGAGACCCGAGACGAGCTGG	941
DB	464 AGCCCCACCTTACACAGGAGCCCTTCGACCTTCAGCTTCGGGAGACCCGAGACGAGCTGG	523
QY	942 AACTGAACCGGAGAGTGCCTGCGCGCACCCCAAACAGAACCATCTTGCACAGTGA	1001
DB	524 AACTGAACCGGAGAGTGCCTGCGCGCACCCCAAACAGAACCATCTTGCACAGTGA	583
QY	1002 TGGATAGTGCAGAGCTGGGCGGCGCCCTTCGCCCCCGACAGATTAATCTCGGGCATACGGCCA	1066
DB	584 TGGATAGTGCAGAGCTGGGCGGCGCCCTTCGCCCCCGACAGATTAATCTCGGGCATACGGCCA	643
QY	1062 CGTGTCTAGGGAGCGGGGGGCGATGAGAGGGGCGCGCCCACTTACGACAGGTCATCG	1121

Db	644	CGTGTACGGGAGCGCGGGGGGCATATGAGAGGGGGCCGGCCCACTTAACAGCAAGGTCAATCG	703
Qy	1122	GGCACTACCCGGGGGTCTCTTTCAGACACACAGAGAGAGATGGGGCCGGCTCTTTGTG	1181
Db	704	GCACACTACCCGGGGGTCTCTTTCAGACACAGAGAGAGATGGGGCCGGCTCTTTGTG	763
Qy	1182	AGGGGACCCGGCTCCACACACACATCGGGCCCTTAGAGAGGCAAGCCATCTGAGACA	1241
Db	764	AGGGGACCCGGCTCCACACACACATCGGGCCCTTAGAGAGGCAAGCCATCTGAGACA	823
Qy	1242	AAGAGAAAGATAAACAGAAAGGACACCTCTCTAGAGGTCCCGAGGGGGCCGGCTGGGG	1301
Db	824	AAGAGAAAGATAAACAGAAAGGACACCTCTCTAGAGGTCCCGAGGGGGCCGGCTGGGG	883
Qy	1302	CTGCGTAGGTGAAAAAGGAGC	1321
Db	884	CTGCGTAGGTGAAAAAGGAGC	903
RESULT 15			
LOCUS	CS130842	4531 bp	DNA
DEFINITION	Sequence 128 from Patent WO2005064009.	linear	PAT 02-AUG-2005
ACCESSION	CS130842		
VERSION	CS130842.1	GI:71792912	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1		
TITLE	Oerntofc,T.F.		
JOURNAL	Classification of cancer Patent: WO 2005064009-A 128 14-JUL-2005;		
FEATURES	Aros Applied Biotechnology Aps (DK)		
source	Location/Qualifiers		
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	/note="transmembrane, prostate androgen induced RNA (r"		
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Query Match	60.6%; Score 800; DB 6; Length 4531;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches	800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	522	CGAGCTGGAAGTTTGTTCATCATCATCATCATCTGTGTGTATGATGATGTGTGTGTG	581
Db	104	CGAGCTGGAAGTTTGTTCATCATCATCATCATCTGTGTGTATGATGATGTGTGTG	163
Qy	582	TGATACAGTCCCTGTGAGCCATCAAGCTGTGCA CGGTCCTTCAACGCGGACCA	641
Db	164	TGATACAGTCCCTGTGAGCCATCAAGCTGTGTGCA CGGTCCTTCAACGCGGACCA	223
Qy	642	GCCAGGGGCGAGAGAGAGATGCGCTGTCTCTGAAAGATGCTCTGTGGCCTTGAGGA	701
Db	224	GCCAGGGGCGAGAGAGAGATGCGCTGTCTCTGAAAGATGCTCTGTGGCCTTGAGGA	283
Qy	702	GCAACGTGTCAAGCAACGGAATCCAGAGCGCAGAGCTTACGCCCTTGAGCCACCG	761
Db	284	GCAACGTGTCAAGCAACGGAATCCAGAGCGCAGAGCTTACGCCCTTGAGCCACCG	343
Qy	762	ACCGGCTGGCGGTGCCCGCTTCCGCGCCAGCGGAGCGCTTCCACGGCTTCAAGCCCACT	821
Db	344	ACCGGCTGGCGGTGCCCGCTTCCGCGCCAGCGGAGCGCTTCCACGGCTTCAAGCCCACT	403
Qy	822	ATTCGTACTGTGAGACAGAGATCACTGTCCACCCACCACTTCGTGTCAAGCGGGAGG	881
Db	404	ATTCGTACTGTGAGACAGAGATCACTGTCCACCCACCACTTCGTGTCAAGCGGGAGG	463
Qy	882	AGCCCCACCTTACCAAGGGGCCCTTGACCTTCAGCTTGGGACCCGAGACAGACGCTGG	941

Db	464	AGCCCCACCCCTTACCAAGGACCCTTGCACCTTCCAGCTTGGGAGCCCGGACGACGACGCTGG	523
QY	942	AACTGAACCGGAGATCGGTGCGGCAACCCCAACAGAACCATCTTTCAGACGTGACTTGA	1001
Db	524	AACTGAACCGGAGATCGGTGCGGCAACCCCAACAGAACCATCTTTCAGACGTGACTTGA	583
QY	1002	TGATTAATGTCACAGGCTTGGGCGGCCCCCTTGCCTCCCAAGACTAACTCGGCGATCAGCGCCA	1061
Db	584	TGATTAATGTCACAGGCTTGGGCGGCCCCCTTGCCTCCCAAGACTAACTCGGCGATCAGCGCCA	643
QY	1062	CGTCTAATGCGACAGGCGGCGGCGCATTGGAGGGGCGCGGCCCACTTACAGGAGGTCAATCG	1121
Db	644	CGTCTAATGCGAGGCGGCGGCGCATTGGAGGGGCGCGGCCCACTTACAGGAGGTCAATCG	703
QY	1122	GCCACTACCGCGGGGTCTCTCTTCCAGACGACGACGACGTGGGCGCCTCTTTCGTGG	1181
Db	704	GCCACTACCGCGGGGTCTCTCTTCCAGACGACGACGACGACGTGGGCGCCTCTTTCGTGG	763
QY	1182	AGGGGACCCGGCTTCACACACACACACATGCGCGCCCTTAGAGAGCGACGCCATCTGGAGCA	1241
Db	764	AGGGGACCCGGCTTCACACACACACACATGCGCGCCCTTAGAGAGCGACGCCATCTGGAGCA	823
QY	1242	AAGGAAGATTAACAGAAAGGACACCTCTCTTAGGCTCCCAAGGGGGGCTCGGGCTTGGGG	1301
Db	824	AAGGAAGATTAACAGAAAGGACACCTCTCTTAGGCTCCCAAGGGGGGCTCGGGCTTGGGG	883
QY	1302	CTGCGTAGGTGAAGAGGACG 1321	
Db	884	CTGCGTAGGTGAAGAGGACG 903	

	RESULT 16			
CS130841	CS130841	4538 bp	DNA	linear PAT 02-AUG-2005
LOCUS	Sequence 127 from Patent WO2005064009.			
DEFINITION	CS130841			
ACCESSION	CS130841			
VERSION	CS130841.1			
KEYWORDS	GI:71792911			
SOURCE	.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Homo.			
REFERENCE	1			
AUTHORS	O'Brien,T.F.			
TITLE	Classification of cancer			
JOURNAL	Patent: WO 2005064009-A 127 14-JUL-2005;			
	Aros Applied Biotechnology APS (DK)			
FEATURES	Location/Qualifiers			
source	1..4538			
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	Query Match	60.6%; Score 800; DB 6; Length 4538;		
	Best Local Similarity 100.0%; Pred. No. 0;			
	Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Gy	522 CGAGCTGAGATTGTTCATCATCATCATCGTGTTGGTAGTSGTAGTGGTGG 581			
Db	111 CGAGCTGAGATTGTTCATCATCATCATCGTGTTGGTAGTSGTAGTGGTGG 170			
Gy	582 TGATCAGTGCCTGCTGAAGCCACTCAACAAGCTGTCTGACAGGTCCTTCATCAGCCGGCAC 641			
Db	171 TGATCAGTGCCTGCTGAGCCACTCAACAAGCTGTCTGACAGGTCCTTCATCAGCCGGCAC 230			
Gy	642 GCCAGGGGCCGAGAGAGAAGATGCCCTGTCTCAGAAGAGATGCTGTGGCCCTCGAGA 701			
Db	231 GCCAGGGGCCGAGAGAGAAGATGCCCTGTCTCAGAAGAGATGCTGTGGCCCTCGAGA 290			

QY 702 GCACAGTGTGACGGAAGAAATCCAGAGCCGACAGTCTACGCCCGCTCGGCCACCG 761  
DB 291 GCAAGTGTGACGGAAGAAATCCAGAGCCGACAGTCTACGCCCGCTCGGCCACCG 350  
QY 762 ACCGCTGCGCGTGCCTCTTCCGCGGAGCGCTTCCACGCTTCCAGCCACCT 821  
DB 351 ACCGCTGCGCGTGCCTCTTCCGCGGAGCGCTTCCACGCTTCCAGCCACCT 410  
QY 822 ATCCGTACTCTGACGACGAGATGACCTTCCACCCACCATCTCTGTTCAGACGGGAGG 881  
DB 411 ATCCGTACTCTGACGACGAGATGACCTTCCACCCACCATCTCTGTTCAGACGGGAGG 470  
QY 882 AGCCCCACCTTACGAGAGGCGCTTCCACCCACCATCTCTGTTCAGACGGGAGG 941  
DB 471 AGCCCCACCTTACGAGAGGCGCTTCCACCCACCATCTCTGTTCAGACGGGAGG 530  
QY 942 AACTGAACCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 1001  
DB 531 AACTGAACCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 590  
QY 1002 TGGATAGTGTGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 1061  
DB 591 TGGATAGTGTGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 650  
QY 1062 CGTGTCTACGCGACGCGCGCGCGCATGAGAGGCGCGCGCCCACTACAGCGAGTCACTG 710  
DB 651 CGTGTCTACGCGACGCGCGCGCGCATGAGAGGCGCGCGCCCACTACAGCGAGTCACTG 710  
QY 1122 GCCACTACCGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 1181  
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QY 1182 AGGGGACCGCGTCTCAACCAACATCTGCGCCCTTACAGAGCGGACCATCTGAGCA 1241  
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QY 1242 AAGAGAGGATTAACAGAAAGGACACCTCTCTTACAGAGCGGAGCGCGCTGAGG 1301  
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QY 1302 CTGCGTAGGTGAAAAGGCG 1321  
DB 891 CTGCGTAGGTGAAAAGGCG 910

RESULT 17  
AR336831 759 bp DNA linear PART 17-AUG-2003  
LOCUS AR336831  
DEFINITION Sequence 2 from patent US 6566130.  
ACCESSION AR336831  
VERSION AR336831.1 GI:33722681  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 759)  
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.  
TITLE Androgen-regulated gene expressed in prostate tissue  
JOURNAL Patent: US 6566130-A 2 20-MAY-2003;  
Henry M. Jackson Foundation for the Advancement of Military  
Medicine; Rockville, MD  
FEATURES  
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1..759  
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Query Match 57.2%; Score 755; DB 6; Length 759;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGGAGCTGAGAGTTTGTTCAGATCATCATCTGTGTGAGTGAAGTGAAGTGTGTG 581

DB 5 CGGAGCTGAGAGTTTGTTCAGATCATCATCTGTGTGAGTGAAGTGAAGTGTGTG 64  
QY 582 TGATCAGTGTGCTCTGAGCCACTACAGAGTGTGTGACGGTCTTATCAGCCGGACA 641  
DB 65 TGATCAGTGTGCTCTGAGCCACTACAGAGTGTGTGACGGTCTTATCAGCCGGACA 124  
QY 642 GCCAGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGTGTGTGAGTGTGTGAGG 701  
DB 125 GCCAGGGCGGAGAGAGAGATGCTCTGTCTCAGAGAGTGTGTGAGTGTGTGAGG 184  
QY 702 GCACAGTGTGACGGAAGAAATCCAGAGCCGACAGTCTACGCCCGCTCGGCCACCG 761  
DB 185 GCAAGTGTGACGGAAGAAATCCAGAGCCGACAGTCTACGCCCGCTCGGCCACCG 244  
QY 762 ACCGCTGCGCGTGCCTCTTCCGCGGAGCGCTTCCACGCTTCCAGCCACCT 821  
DB 245 ACCGCTGCGCGTGCCTCTTCCGCGGAGCGCTTCCACGCTTCCAGCCACCT 304  
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QY 882 AGCCCCACCTTACGAGAGGCGCTTCCACCCACCATCTCTGTTCAGACGGGAGG 941  
DB 365 AGCCCCACCTTACGAGAGGCGCTTCCACCCACCATCTCTGTTCAGACGGGAGG 424  
QY 942 AACTGAACCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 1001  
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QY 1002 TGGATAGTGTGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 1061  
DB 485 TGGATAGTGTGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 544  
QY 1062 CGTGTCTACGCGACGCGCGCGCATGAGAGGCGCGCGCCCACTACAGCGAGTCACTG 1121  
DB 545 CGTGTCTACGCGACGCGCGCGCATGAGAGGCGCGCGCCCACTACAGCGAGTCACTG 604  
QY 1122 GCCACTACCGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 1181  
DB 605 GCCACTACCGCGGAGTGTGCGGACCGCCCAACCAAGAACATCTTTCAGACGTGACTGA 664  
QY 1182 AGGGGACCGCGTCTCAACCAACATCTGCGCCCTTACAGAGCGGACCATCTGAGCA 1241  
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QY 1242 AAGAGAGGATTAACAGAAAGGACACCTCTCTTACAGAGCGGAGCGCGCTGAGG 1301  
DB 725 AAGAGAGGATTAACAGAAAGGACACCTCTCTTACAGAGCGGAGCGCGCTGAGG 890

RESULT 18  
BD272494 969 bp DNA linear PART 17-JUL-2003  
LOCUS BD272494  
DEFINITION Secreted proteins and nucleic acids encoding them.  
ACCESSION BD272494  
VERSION BD272494.1 GI:33082262  
KEYWORDS JP 2002539773-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 969)  
AUTHORS Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Frazer,C.C.  
TITLE Secreted proteins and nucleic acids encoding them  
JOURNAL MILLENNIUM PHARMACEUTICALS INC  
OS Homo sapiens (human)  
PN JP 2002539773-A/3  
PD 26-NOV-2002  
PF 01-MAR-2000 JP 2000602247  
PR 01-MAR-1999 US 60/122458



Qy		1002	TGATATAGTGCACAGGTGGGGCGCCCTTCGACCAAGTAACCTCGGGATCATAGCGACA	1068
Db		612	TGAATAGTGCCAGAGGTGGGGCGCCCTTCGCCCCCGAGCATACTCGGGATCATAGCGCCA	671
Qy		1062	CGTCTACTACGACGAGCGGGCGGCATATGAGGAGGGCGCGGCCCACTTACACCGAAGGTCAATCG	1121
Db		672	CGTCTACTACGACGAGCGGGCGGCATATGAGGAGGGCGCGGCCCACTTACACGAGGTCAATCG	731
Qy		1122	GCCACTACCCGGGGGTCTCTCTTTCCAGCACACGACGACGATGGGGCCGCTCTTCTTGGCTGG	1181
Db		732	GCCACTACCCGGGGGTCTCTCTTCCAGCACACGACGACGATGGGGCGCTCTCTTGGCTGG	791
Qy		1182	AGGGGACCCCGGCTCCACACACACATATCGGGCCCCCTTAGAGAGGGCGACGATCTGAGACA	1241
Db		792	AGGGGACCCCGGCTCCACACACACATATCGGGCCCCCTTAGAGAGGGCGACGATCTGAGACA	851
Qy		1242	AAGAGAAGATTAACAAGAAAGGACACCCTCTTAGAGGTCCCACAGGGGGCGCGCTGGGG	1301
Db		852	AAGAGAAGATTAACAAGAAAGGACACCCTCTTAGAGGTCCCACAGGGGGCGCGCTGGGG	911
Qy		1302	CTGCGTAGGTGAAAAGCGAC	1321
Db		912	CTGCGTAGGTGAAAAGCGAC	931
RESULT 20				
Bd272544.				
LOCUS	Bd272544	1913 bp	DNA	linear
DEFINITION	Secreted proteins and nucleic acids encoding them.			PAT 17-JUL-2003
ACCESSION	Bd272544			
VERSION	Bd272544.1	GI:33082312		
KEYWORDS	JP 2002539773-A/53.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1913)			
AUTHORS	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.			
TITLE	Secreted proteins and nucleic acids encoding them			
JOURNAL	Patent: JP 2002539773-A 53 26-NOV-2002;			
	MILLENNIUM PHARMACEUTICALS INC			
COMMENT	OS Homo sapiens (human)			
	PN JP 2002539773-A/53			
	PD 26-NOV-2002			
	PF 01-MAR-2000 JP 2000602247			
	PR 01-MAR-1999 US 60/122458			
	PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C			
	PI FRASER			
	PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC			
	G01N33/15,			
	PC G01N33/50, G01N33/53, G01N33/56, C12N15/00, C12N5/00 CC			
	Secreted proteins and nucleic acids encoding them FH Key			
	Location/Qualifiers			
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ORIGIN				
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	Best Local Similarity	99.9%; Pred. No. 0;		
	Matches /99; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
Qy	522	CGAGAGCTGAGATTGTTTCAGATCATCATCATCGTGGTGTGATGATGTGATGTGGTGG	581	
Db	150	CGAGAGCTGAGATTGTTTCAGATCATCATCATCGTGGTGTGATGATGTGATGTGGTGG	209	
Qy	582	TGATCACTGCTGCTGAGCCACTACAGCTGTTCAGAGGTCTTCATCTACCGCGGACA	641	

Db	210	TGATCACTGTCCTGCTBAGCCACTACAAAGCTGTCTGACGGTCTTCAATCAGCGGACCA	269
QY	642	GCCAGGGGCGGAGAGAAAGATGCCCTGTCTTCAGAAAGATGCTGTGGCCCTTCGAGA	701
Db	270	GCCAGGGGCGGAGAGAAAGATGCCCTGTCTTCAGAAAGATGCTGTGGCCCTTCGAGA	329
QY	702	GCAAGTGTCAAGGCAAGGAATCCCAAGCCGACAGTCTAGCGCCGCTCGGCCCAACG	761
Db	330	GCAAGTGTCAAGGCAAGGAATCCCAAGCCGACAGTCTAGCGCCGCTCGGCCCAACG	389
QY	762	ACCGCTTGAGCCGCTGCCCGCTTCGCGCCAGGCGGAGCGCTTTCACCGCTTCAGGCCACT	821
Db	390	ACCGCTTGAGCCGCTGCCCGCTTCGCGCCAGGCGGAGCGCTTTCACCGCTTCAGGCCACT	449
QY	822	ATCCGTACTGTCAGACGACGAGATGCACCTTGCCACCCATCTCGCTGTCAAGCGGGAGG	881
Db	450	ATCCGTACTGTCAGACGAGATGCACCTTGCCACCCATCTCGCTGTCAAGCGGGAGG	509
QY	882	AGCCCCACCCCTTACCAAGGCGCCCTGCAACCTCCAGCTTCGGGACCCCGAGCAGACTGG	941
Db	510	AGCCCCACCCCTTACCAAGGCGCCCTGCAACCTCCAGCTTCGGGACCCCGAGCAGACTGG	569
QY	942	AAGTGAACCGGGAGTGGTGGTGGCGCACCCCAACAGAAACCATCTTTCAGACGTGACTGA	1001
Db	570	AAGTGAACCGGGAGTGGTGGTGGCGCACCCCAACAGAAACCATCTTTCAGACGTGACTGA	629
QY	1002	TGAGTATGTCGAGGCTGGGCGGCGCCCTTGCGCCCGCCAGCATGTAATCTCGGGCATGCGCCA	1061
Db	630	TGAGTATGTCGAGGCTGGGCGGCGCCCTTGCGCCCGCCAGCATGTAATCTCGGGCATGCGCCA	689
QY	1062	CGTGTCTAAGGCAAGGCGGCGGCGCATGGAAGGGGCGCGCCCACTTACAGCAGAGGTCAATCG	1121
Db	690	CGTGTCTAAGGCAAGGCGGCGGCGCATGGAAGGGGCGCGCCCACTTACAGCAGAGGTCAATCG	749
QY	1122	GCACTACCCGGGGTCTCTTTCAGAGCACAGCAGACAGTGGGCGCGCTCTTGTCTGG	1181
Db	750	GCACTACCCGGGGTCTCTTTCAGAGCACAGCAGACAGTGGGCGCGCTCTTGTCTGG	809
QY	1182	AGGGGACCCGGGCTCCACCACACACACATCGCGCCCTTACAGAGCGCAGCCATCTGGAGCA	1241
Db	810	AGGGGACCCGGGCTCCACCACACACACATCGCGCCCTTACAGAGCGCAGCCATCTGGAGCA	869
QY	1242	AAGAGAAAGATTAACACGAAGAAGACACCTCTCTAGAGGGTCCCAAGGGGGCGGGGCTGGGG	1301
Db	870	AAGAGAAAGATTAACACGAAGAAGACACCTCTCTAGAGGGTCCCAAGGGGGCGGGGCTGGGG	929
QY	1302	CTGGCTAGTGTAAGAAAGGCGAG 1321	
Db	930	CTGGCTAGTGTAAGAAAGGCGAG 949	

RESULT 21

BD272514

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

669 bp DNA linear PAT 17-JUL-2003

Secreted proteins and nucleic acids encoding chem.

BD272514

BD272514.1 GI:33082282

JP 2002539773-A/23.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (baaes 1 to 969)

Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.

Secreted proteins and nucleic acids encoding chem

Patent: JP 2002539773-A 23 26-NOV-2002;

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002539773-A/23

PD 26-NOV-2002

PF 01-MAR-2000 JP 2000602247

PR 01-MAR-1999 US 60/122458



Query Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
527	CTGGAGTTTGTTCAGATCATCATCATC	56.3%	744	969	0	0	1	0	0
15	CTGGAGTTTGTTCAGATCATCATCATC	99.9%	794	969	0	0	1	0	0
587	ACGTGCTCTGTAAGCCTACCAAGCTG	56.3%	744	969	0	0	1	0	0
75	ACGTGCTCTGTAAGCCTACCAAGCTG	99.9%	794	969	0	0	1	0	0
647	GGGCGGAGAGAGAGATGAGGCTGCTC	56.3%	744	969	0	0	1	0	0
135	GGGCGGAGAGAGAGATGAGGCTGCTC	99.9%	794	969	0	0	1	0	0
707	GTGTGAGCAACGAGATCCAGAGCCGCA	56.3%	744	969	0	0	1	0	0
195	GTGTGAGCAACGAGATCCAGAGCCGCA	99.9%	794	969	0	0	1	0	0
767	CTGGCGGTGCGCGCTTGTGCGCGAGC	56.3%	744	969	0	0	1	0	0
255	CTGGCGGTGCGCGCTTGTGCGCGAGC	99.9%	794	969	0	0	1	0	0
857	TACCTGACGACGAGATGACCTGCGAAC	56.3%	744	969	0	0	1	0	0
315	TACCTGACGACGAGATGACCTGCGAAC	99.9%	794	969	0	0	1	0	0
887	CCACCCTACCAAGGCGCCCTGCAACCT	56.3%	744	969	0	0	1	0	0
375	CCACCCTACCAAGGCGCCCTGCAACCT	99.9%	794	969	0	0	1	0	0
947	AAACGGGAGTCCGTGCGCGCAACCCCA	56.3%	744	969	0	0	1	0	0
435	AAACGGGAGTCCGTGCGCGCAACCCCA	99.9%	794	969	0	0	1	0	0
1007	AGTGCAGGCTGGGGGCGCCCTGCGCCG	56.3%	744	969	0	0	1	0	0
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1067	TACGGCAGCGCGCGCGCATGTGAGGGG	56.3%	744	969	0	0	1	0	0
555	TACGGCAGCGCGCGCGCATGTGAGGGG	99.9%	794	969	0	0	1	0	0
1127	TACCCGGGGTCTCTCTTCCAGACCAAG	56.3%	744	969	0	0	1	0	0
615	TACCCGGGGTCTCTCTTCCAGACCAAG	99.9%	794	969	0	0	1	0	0
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1247	AAAGATTAACAGAAAGACATCCCTCTT	56.3%	744	969	0	0	1	0	0
735	AAAGATTAACAGAAAGACATCCCTCTT	99.9%	794	969	0	0	1	0	0
1307	TAGGTGAAAAGGCAG	56.3%	744	969	0	0	1	0	0

[illegible]











## TITLE

Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  
 Patent: WO 02068579-A 14876 06-SEP-2002;

## JOURNAL

PE Corporation (NY) (US)  
 Location/Qualifiers

1. 600  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 45.4%; Score 600; DB 6; Length 600;  
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 Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

677 GAAAGATGCTGTGACCCCTCGAGAGACAGAGTCCAGCAACGAAATCCAGAGCCGAG 736  
 1 GAAAGATGCTGTGACCCCTCGAGAGACAGAGTCCAGCAACGAAATCCAGAGCCGAG 60  
 737 GTCTACGCGCCGCTCGAGCCACCGACGCTGCGCCCTTCGCCAGCGGAG 796  
 61 GTCTACGCGCCGCTCGAGCCACCGACGCTGCGCCCTTCGCCAGCGGAG 120  
 797 CGCTTCCACCGCTTCCAGCCCACTATCCGTACCTTCAGACAGAAATGACCTGCGACCC 856  
 121 CGCTTCCACCGCTTCCAGCCCACTATCCGTACCTTCAGACAGAAATGACCTGCGACCC 180  
 857 ACCATCTGCTGTGACGCGGAGAGAGCCCACTACAGAGCCCTTCAGAGCCCTTCAG 916  
 181 ACCATCTGCTGTGACGCGGAGAGAGCCCACTACAGAGCCCTTCAGAGCCCTTCAG 240  
 917 CTTCGCGACCCCGAGAGAGAGTGAATGAACCGGAGTCTGCGCGACCCCAAC 976  
 241 CTTCGCGACCCCGAGAGAGAGTGAATGAACCGGAGTCTGCGCGACCCCAAC 300  
 977 AGAACCATTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1036  
 301 AGAACCATTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 1037 ACCAGTAACTCGGGGATCGAGGCAAGCTGCTACGCGAGCGGCGAGCTGAGAGGAGCG 1096  
 361 ACCAGTAACTCGGGGATCGAGGCAAGCTGCTACGCGAGCGGCGAGCTGAGAGGAGCG 420  
 1097 CGGCCACCTAGAGAGAGTCAATCGGCACTACCCGGGCTCTCTTCAGACAGCAG 1156  
 421 CGGCCACCTAGAGAGAGTCAATCGGCACTACCCGGGCTCTCTTCAGACAGCAG 480  
 1157 AGCAGTGGGCGCGCTCTCTTGTGAGGAGAGCCCGCTCCACACACACATTCGGGCC 1216  
 481 AGCAGTGGGCGCGCTCTCTTGTGAGGAGAGCCCGCTCCACACACACATTCGGGCC 540  
 1217 CTAGAGAGGCGGACCTGAGAGCAAGAGATTAACAGAAAGAGACACCTCTCTAG 1276  
 541 CTAGAGAGGCGGACCTGAGAGCAAGAGATTAACAGAAAGAGACACCTCTCTAG 600

RESULT 29  
 AF305426 61505 bp DNA linear PRI 12-OCT-2001  
 LOCUS AF305426  
 DEFINITION Homo sapiens solid tumor-associated 1 protein (STAG1/PMEP1) gene,  
 complete cds.  
 ACCESSION AF305426  
 VERSION AF305426.1 GI:15824468  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 (bases 1 to 61505)  
 REFERENCE  
 Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.  
 Identification and characterization of a novel gene, STAG1,

## JOURNAL

up-regulated in renal cell carcinoma and other solid tumours  
 Unpublished  
 2 (bases 1 to 61505)  
 Rae,F.K., Hooper,J.D., Nicol,D.L. and Clements,J.A.

## AUTHORS

Submitted (13-SEP-2000) Centre for Molecular Biotechnology,  
 Queensland University of Technology, 2 George St, Brisbane, QLD  
 4001, Australia

## JOURNAL

## TITLE

Location/Qualifiers

1. 61505  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="20"  
 /map="20q13.2-q13.33"  
 1. 61505  
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729 AGCCGAGGTGAGCCCGGCTGCGCCACCGACCGGCTGCGCGCTTCGCGCC 788  
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 789 AGCCGAGGTGAGCCCGGCTGCGCCACCGACCGGCTGCGCGCTTCGCGCC 848  
 57363 AGCCGAGGTGAGCCCGGCTGCGCCACCGACCGGCTGCGCGCTTCGCGCC 57422  
 849 TGCCACCCACCATCTGCTGTCAAGCGGAGAGAGCCCGACCTTACAGAGGCGCTTGA 908  
 57423 TGCCACCCACCATCTGCTGTCAAGCGGAGAGAGCCCGACCTTACAGAGGCGCTTGA 57482  
 909 CCTTCAGCTTGGGAGCCCGAGAGAGCTGGAATGAACCGGAGAGTTCGGCGGAC 968  
 57483 CCTTCAGCTTGGGAGCCCGAGAGAGCTGGAATGAACCGGAGAGTTCGGCGGAC 57542  
 969 CCCCAAGAGAACATCTTGAAGAGTCACTGATGATGATGATGATGATGATGATGATGAT 1028  
 57543 CCCCAAGAGAACATCTTGAAGAGTCACTGATGATGATGATGATGATGATGATGATGAT 57602  
 1029 GCCCCCGAGAGTAACTCGGGCATCAAGCGGCAAGTGTACAGCGCGCGCGCGATGG 1088  
 57603 GCCCCCGAGAGTAACTCGGGCATCAAGCGGCAAGTGTACAGCGCGCGCGCGATGG 57662  
 1089 AGGGGCG 1148  
 57663 AGGGGCG 57722  
 1149 ACCAGCAGAGAGTGGGCG 1208  
 57723 ACCAGCAGAGAGTGGGCG 57782  
 1209 TCGCGCCCTTGAAGAGCGCAGCATCTGAGCAAGAGAGATTAACAGAAAGAGACACC 1268  
 57783 TCGCGCCCTTGAAGAGCGCAGCATCTGAGCAAGAGAGATTAACAGAAAGAGACACC 57842

## ORIGIN

Query Match 44.9%; Score 593; DB 8; Length 61505;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-283;  
 Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 30
HS718J7/c
LOCUS
DEFINITION
Human DNA
130435 bp
DNA
linear
PRI 18-MAY-2005
ACCESSION
AL035541
VERSION
HTG; C200cf113; Cpg island; CTCFL; DLM-1; macrophage protein; PCK1;
KEYWORDS
phosphoenolpyruvate carboxykinase; TMEPAI; transmembrane
protein; ZBP1.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 130435)
REFERENCE
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Dec 5, 2000 this sequence version replaced gi:10198628.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone configs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
RP4-718J7 is from the library RPCT-4 constructed by the group of
Pleier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
-----Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
FEATURES
source
1..130435
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/db_xref="taxon:9606"
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/map="q13.31-13.33"
/clone="RP4-718J7"
/clone_1lb="RPCT-4"
1
/note="Clone left end. RP4-718J7"
join(complement(871..972),
complement(ALT60176..3:56872)),

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polya\_1 site











Query Match 22.9%; Score 302; DB 6; Length 693;  
Best Local Similarity 100.0%; Pred. No. 1.2e-118;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 885 CCCACCCCTTACAGAGGCGCCCTTGACACCTTCCAGCTTCGGAGACCCCGAGCAGAGCTGAGAC 944  
DB 587 CCCACCCCTTACAGAGGCGCCCTTGACACCTTCCAGCTTCGGAGACCCCGAGCAGAGCTGAGAC 528

QY 945 TGAACCGGAGTCGGTGGCGGCAACCCCAACAGAACCATCTTGACAGTGAACCTGATGG 1004  
DB 527 TGAACCGGAGTCGGTGGCGGCAACCCCAACAGAACCATCTTGACAGTGAACCTGATGG 468

QY 1005 ATATGTCGACAGCTGGGCGGCGCCCTTGACAGTGAACCTGAGGAGTGAACCTGATGG 1064  
DB 467 ATATGTCGACAGCTGGGCGGCGCCCTTGACAGTGAACCTGAGGAGTGAACCTGATGG 408

QY 1065 GCTACGGGAGGCGGCGGCGGCAATGAGAGGCGCGCCCACTTACAGAGGAGTGAACCTGATGG 1124  
DB 407 GCTACGGGAGGCGGCGGCGGCAATGAGAGGCGCGCCCACTTACAGAGGAGTGAACCTGATGG 348

QY 1125 ACTACCGGAGTCTCTCTTCCAGACACAGAGAGTGGCGCGCTCTCTTGTGAGAG 1184  
DB 347 ACTACCGGAGTCTCTCTTCCAGACACAGAGAGTGGCGCGCTCTCTTGTGAGAG 288

QY 1185 GG 1186  
DB 287 GG 286

RESULT 35  
BD226320 812 bp DNA linear PAT 17-JUL-2003  
LOCUS BD226320  
DEFINITION Pancreatic cancer tissue-origin human nucleic acid sequence.  
ACCESSION BD226320.1 GI:33036090  
VERSION JP 2002512795-A/105  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 812)  
Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and  
Rosenthal,A.  
Pancreatic cancer tissue-origin human nucleic acid sequence  
Patient: JP 2002512795-A/105 08-MAY-2002;  
METAGEN GSEBLSCHAFT FUER GENOM FORSCHUNG MBH  
OS Homo sapiens (human)  
PN JP 2002512795-A/105  
PD 08-MAY-2002  
PF 19-APR-1999 JP 2000546002  
PR 28-APR-1998 DE 198 20 190.7  
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,  
PI EDGAR DAHL,  
PI ANDRE ROSENTHAL  
PC C12N15/09,A61K38/00,A61K48/00,A61P1/18,A61P35/00,C07K14/435,  
PC C07K16/18,  
PC C12N5/10,C12P21/02,C12P21/08,C12N15/00,A61K37/02,C12N5/00 CC  
Pancreatic cancer tissue-origin human nucleic acid sequence FH  
Key Location/Qualifiers  
FT source 1..812  
FT location/Qualifiers  
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location/Qualifiers  
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ORIGIN  
Query Match 20.5%; Score 271; DB 6; Length 812;  
Best Local Similarity 99.7%; Pred. No. 3.4e-123;  
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCACGTGCTGCTGAGGCACTTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 644  
DB 426 TCACGTGCTGCTGAGGCACTTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 485

QY 645 AGGGGCGGAGGAGAGGATGCTGTCTCAGAAAGATGCTGTGGCCCTCGGAGAGCA 704  
DB 486 AGGGGCGGAGGAGAGGATGCTGTCTCAGAAAGATGCTGTGGCCCTCGGAGAGCA 545

QY 705 CAGTGTGAGCAACGAAATCCAGAGCCGAGGTCTTACGCTCCGCTCGGACCAAGCC 764  
DB 546 CAGTGTGAGCAACGAAATCCAGAGCCGAGGTCTTACGCTCCGCTCGGACCAAGCC 605

QY 765 GCTTGGCGCTGCGGCGCTTGGCCAGGAGGAGGCTTTCACGCGCTTCAGGCCACTATC 824  
DB 606 GCTTGGCGCTGCGGCGCTTGGCCAGGAGGAGGCTTTCACGCGCTTCAGGCCACTATC 665

QY 825 GCTACCTGACAGCAGAGATGACCTTGCCACCCACATCTGCTGTGAGAGCGGAGAGC 884  
DB 666 GCTACCTGACAGCAGAGATGACCTTGCCACCCACATCTGCTGTGAGAGCGGAGAGC 725

QY 885 CCCACCCCTTACAGAGGCGCCCTG 906  
DB 726 CCCACCCCTTACAGAGGCGCCCTG 747

RESULT 36  
AX011709 812 bp DNA linear PAT 06-SEP-2000  
LOCUS AX011709  
DEFINITION Sequence 107 from Patent WO9955858.  
ACCESSION AX011709  
VERSION AX011709.1 GI:9998233  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1  
Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and  
Pilarsky,C.  
Human nucleic acid sequences obtained from pancreas tumor tissue  
JOURNAL  
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN  
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUNG  
(DE); PILARSKY CHRISTIAN (DE)  
Location/Qualifiers  
source 1..812  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"

ORIGIN  
Query Match 20.5%; Score 271; DB 6; Length 812;  
Best Local Similarity 99.7%; Pred. No. 3.4e-123;  
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCACGTGCTGCTGAGGCACTTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 644  
DB 426 TCACGTGCTGCTGAGGCACTTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 485

QY 645 AGGGGCGGAGGAGAGGATGCTGTCTCAGAAAGATGCTGTGGCCCTCGGAGAGCA 704  
DB 486 AGGGGCGGAGGAGAGGATGCTGTCTCAGAAAGATGCTGTGGCCCTCGGAGAGCA 545

QY 705 CAGTGTGAGCAACGAAATCCAGAGCCGAGGTCTTACGCTCCGCTCGGACCAAGCC 764  
DB 546 CAGTGTGAGCAACGAAATCCAGAGCCGAGGTCTTACGCTCCGCTCGGACCAAGCC 605

QY 765 GCTTGGCGCTGCGGCGCTTGGCCAGGAGGAGGCTTTCACGCGCTTCAGGCCACTATC 824  
DB 606 GCTTGGCGCTGCGGCGCTTGGCCAGGAGGAGGCTTTCACGCGCTTCAGGCCACTATC 665

QY 825 CGTACTGACAGACGAGATCGACCTGCGACCCACCATCTCGCTGTCAGACGGGGAGAGC 884  
DB 666 CGTACTGACAGACGAGATCGACCTGCGACCCACCATCTCGCTGTCAGACGGGGAGAGC 725  
QY 885 CCGGACCTGACGAGGAGCCCTG 906  
DB 726 CCGGACCTGACGAGGAGCCCTG 747

## RESULT 37

LOCUS CQ976479 310 bp DNA linear PAT 19-JAN-2005  
DEFINITION Sequence 170 from Patent WO2004113571.  
ACCESSION CQ976479  
VERSION CQ976479.1 GI:57975807  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.  
TITLE Prostate specific genes and the use thereof as targets for prostate  
cancer therapy and diagnosis  
JOURNAL Patent: WO 2004113571-A 170 29-DEC-2004;  
Exonhit Therapeutics S.A. (FR)  
FEATURES  
source location/Qualifiers  
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## ORIGIN

Query Match 15.8%; Score 209; DB 6; Length 310;  
Best Local Similarity 100.0%; Pred. No. 2.5e-92;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CCGAGCTGAGTTGTTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 581  
DB 102 CCGAGCTGAGTTGTTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 161  
QY 582 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGCTCTTCATCAGCCGAC 641  
DB 162 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGCTCTTCATCAGCCGAC 221  
QY 642 GCCAGGGGGGAGAGAGAGATGCCCTGCTCCAGAGAGATGCCGTGGCCCTCGGAGA 701  
DB 222 GCCAGGGGGGAGAGAGAGATGCCCTGCTCCAGAGAGATGCCGTGGCCCTCGGAGA 281  
QY 702 GCACAGTGTCAAGCAACGGAATCCAGAG 730  
DB 282 GCACAGTGTCAAGCAACGGAATCCAGAG 310

## RESULT 38

LOCUS CQ976481 529 bp DNA linear PAT 19-JAN-2005  
DEFINITION Sequence 172 from Patent WO2004113571.  
ACCESSION CQ976481  
VERSION CQ976481.1 GI:57975809  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.  
TITLE Prostate specific genes and the use thereof as targets for prostate  
cancer therapy and diagnosis  
JOURNAL Patent: WO 2004113571-A 172 29-DEC-2004;  
Exonhit Therapeutics S.A. (FR)

## FEATURES

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/db\_xref="taxon:9606"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.5e-92;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CCGAGCTGAGTTGTTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 581  
DB 209 CCGAGCTGAGTTGTTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 150  
QY 582 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGCTCTTCATCAGCCGAC 641  
DB 149 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGCTCTTCATCAGCCGAC 90  
QY 642 GCCAGGGGGGAGAGAGATGCCCTGCTCCAGAGAGATGCCGTGGCCCTCGGAGA 701  
DB 89 GCCAGGGGGGAGAGAGATGCCCTGCTCCAGAGAGATGCCGTGGCCCTCGGAGA 30  
QY 702 GCACAGTGTCAAGCAACGGAATCCAGAG 730  
DB 29 GCACAGTGTCAAGCAACGGAATCCAGAG 1

## RESULT 39

LOCUS CQ976478 579 bp DNA linear PAT 19-JAN-2005  
DEFINITION Sequence 169 from Patent WO2004113571.  
ACCESSION CQ976478  
VERSION CQ976478.1 GI:57975806  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.  
TITLE Prostate specific genes and the use thereof as targets for prostate  
cancer therapy and diagnosis  
JOURNAL Patent: WO 2004113571-A 169 29-DEC-2004;  
Exonhit Therapeutics S.A. (FR)  
FEATURES  
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## ORIGIN

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DB 431 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGCTCTTCATCAGCCGAC 490  
QY 642 GCCAGGGGGGAGAGAGATGCCCTGCTCCAGAGAGATGCCGTGGCCCTCGGAGA 701  
DB 491 GCCAGGGGGGAGAGAGATGCCCTGCTCCAGAGAGATGCCGTGGCCCTCGGAGA 550  
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Dn	1 CACGGTCCTTATCATGCGCGCACAGCCGAGGGGCGGAGGAGGAAGATCCCC 51					
RESULT 46						
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LOCUS	BD272547					
DEFINITION	Secreted proteins and nucleic acids encoding them.					
ACCESSION	BD272547					
VERSION	BD272547.1 GI:33082315					
KEYWORDS	JP 2002539773-A/56.					
SOURCE	Mus sp.					
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Frazer,C.C. Secreted proteins and nucleic acids encoding them Patent: JP 2002539773-A 56 26-NOV-2002; MILLENNIUM PHARMACEUTICALS INC					
AUTHORS	TITLE					
JOURNAL						
COMMENT	OS Mus sp. (mouse) PN JP 2002539773-A/56 PD 26-NOV-2002 PF 01-MAR-2000 JP 20006072247 PR 01-MAR-1999 US 60/122458 PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C PI PC FRASER PC C12N5/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC GO1N3/15, PC GO1N3/50, GO1N3/53, GO1N3/53, GO1N3/56, C12N15/00, C12N5/00 CC Secreted proteins and nucleic acids encoding them FH Key Location/Qualifiers					
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Beech Local Similarity	100.0%;	Pred.	No. 3.4e-10;			
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Dn	271 GGGAGGAGACCCCAACCCTACGAGGGCCCTGCACCTTCAGACT 314					
RESULT 47						
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LOCUS	BD272546					
DEFINITION	Secreted proteins and nucleic acids encoding them.					
ACCESSION	BD272546					
VERSION	BD272546.1 GI:33082314					
KEYWORDS	JP 2002539773-A/55.					
SOURCE	Mus sp.					
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 484) Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Frazer,C.C. Secreted proteins and nucleic acids encoding them Patent: JP 2002539773-A 55 26-NOV-2002; MILLENNIUM PHARMACEUTICALS INC					

COMMENT	OS	Mus sp. (mouse)	JP 2002539773-A/55
	PN	26-NOV-2002	2000602247
	PF	01-MAR-2000	JP 2000602247
	PR	01-MAR-1999	US 60/122458
	PI	THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER	
	PC	C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC	
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	PC	GOIN33/50, GOIN33/53, GOIN33/53, GOIN33/566, C12N15/00, C12N5/00	
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	DEFINITION	Secreted proteins and nucleic acids encoding them.	
	ACCESSION	BD272535	
	VERSION	BD272535.1 GI:33082303	
	KEYWORDS	JP 2002539773-A/44.	
	SOURCE	Mus sp.	
	ORGANISM	Mus sp.	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		1 (bases 1 to 648)	
	REFERENCE	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.	
	AUTHORS	Secreted proteins and nucleic acids encoding them	
	TITLE	Patent: JP 2002539773-A 44 26-NOV-2002;	
	JOURNAL	MILLENNIUM PHARMACEUTICALS INC	
	COMMENT	OS Mus sp. (mouse)	
		PN JP 2002539773-A/44	
		PD 26-NOV-2002	
		PF 01-MAR-2000 JP 2000602247	
		PR 01-MAR-1999 US 60/122458	
		PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER	
		PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC	
		GOIN33/15,	
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95	32	2.4	1964	4	AA135267	Probe #39	c 168	29	2.2	4122	10	ACC72793	Acc72793 Human can
96	32	2.4	1964	4	ABA45134	Human bre	c 169	29	2.2	4122	11	ADN95504	Adn95504 Human BRC
97	32	2.4	1964	4	ABA25310	Probe #37	c 170	29	2.2	4122	12	ADP26912	Adp26912 Human N-C
98	32	2.4	1964	4	AAK29307	Human bon	c 171	29	2.2	4122	14	AD226570	Ad226570 Human N-C
99	32	2.4	1964	4	AAK03841	Human bra	c 172	29	2.2	4122	15	AEB35167	Aeb35167 Human Gef
100	32	2.4	1964	4	ABS28927	Human liv	c 173	29	2.2	4136	5	AA578503	Aa578503 Human enco
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106	31	2.3	645	4	AB126561	Oligonuc1	c 179	28	2.1	251	6	ABV95011	Abv95011 Human pan
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109	31	2.3	2332	10	ADB62546	Human CDN	c 182	28	2.1	362	14	ADV77137	Adv77137 Huntingto
110	31	2.3	2808	4	ABL26560	Genomic s	c 183	28	2.1	381	4	ABL41662	Ab141662 Nucleotid
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112	31	2.3	12620	4	AB16691	DNA enco	c 185	28	2.1	504	4	ABL41663	Ab141663 Nucleotid
113	30	2.3	2109	5	AA581477	Human bre	c 186	28	2.1	515	2	AAK18930	Aax18930 Human hun
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115	29	2.2	401	4	AA135443	Probe #41	c 188	28	2.1	600	8	AB281762	Ab281762 Exon 1 of
116	29	2.2	401	4	ABA45299	Human bre	c 189	28	2.1	614	8	AB281762	Ab281762 Huntingto
117	29	2.2	401	4	ABA25470	Probe #39	c 190	28	2.1	636	9	ADA49298	Ada49298 Maize gen
118	29	2.2	401	4	AAK29492	Human bon	c 191	28	2.1	636	11	ACL344692	Ad344692 Rice abio
119	29	2.2	401	4	AAK29492	Human bon	c 192	28	2.1	636	12	ADU44871	Ad44871 Plant CDN
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121	29	2.2	401	4	ABS29116	Human liv	c 194	28	2.1	700	3	AAA37651	Aaa37651 FMR1 gene
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123	29	2.2	401	6	AB804041	Human gen	c 196	28	2.1	729	6	AB032811	Abq32811 Oligonuc1
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131	29	2.2	446	4	AA842140	Human liv	c 204	28	2.1	774	13	ADS92623	Ad92623 Chitinase
132	29	2.2	446	5	AA108921	Probe #89	c 205	28	2.1	774	13	ADS82653	Ad82653 Chitinase
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142	29	2.2	1406	13	ADS31839	Human fib	c 215	28	2.1	1061	13	AEB66996	Aeb66996 Rice geno
143	29	2.2	1466	13	ADU18046	Human can	c 216	28	2.1	1061	13	ADX33157	Adx33157 Plant ful
144	29	2.2	1546	10	AAAD63206	Human DNA	c 217	28	2.1	1077	13	ADX32647	Adx32647 Plant ful
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148	29	2.2	1546	13	ADP25099	Breast ca	c 221	28	2.1	1138	13	ADX59637	Adx59637 Plant ful
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162	29	2.2	3131	12	ADQ19443	Human sof	c 235	28	2.1	2145	14	ADY15693	Ady15693 DNA enco
163	29	2.2	3131	14	ADX07414	Cyclin-de	c 236	28	2.1	2145	14	ADY16190	Ady16190 DNA enco
164	29	2.2	3266	5	AD162149	Human ova	c 237	28	2.1	2145	14	ADY19857	Ady19857 DNA enco
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265	28	2.0	514	6	ABQ32463	338	26	2.0	581	6	ABQ15880	Abq15880 Oligonuc
266	28	2.0	514	6	ABQ32462	339	26	2.0	603	4	AA528166	Aa528166 DNA enco
267	28	2.0	581	6	ABQ15810	340	26	2.0	603	8	ACA03383	AcA03383 Genomic
268	28	2.0	581	6	ABQ15811	341	26	2.0	603	9	ADP96731	Adp96731 Novel lun
269	28	2.0	582	13	ADR31620	342	26	2.0	603	10	ADG41362	Adg41362 Human res
270	28	2.0	598	12	ADN30328	343	26	2.0	603	11	ADG41362	Adg41362 Human res
271	28	2.0	598	14	AEA08537	344	26	2.0	603	11	ADG41362	Adg41362 Human res
272	28	2.0	615	10	ADK56171	345	26	2.0	621	11	ACL97136	ACL97136 Human res
273	28	2.0	820	10	ADD17321	346	26	2.0	621	11	ACL97136	ACL97136 Human res
274	28	2.0	820	10	ADK57273	347	26	2.0	621	11	ACL97136	ACL97136 Human res
275	28	2.0	820	10	ADK57273	348	26	2.0	621	11	ACL97136	ACL97136 Human res
276	28	2.0	820	10	ADK57273	349	26	2.0	621	11	ACL97136	ACL97136 Human res
277	28	2.0	900	5	AA587781	350	26	2.0	641	12	AD159337	Ad159337 Wheat ser
278	28	2.0	900	5	AA587781	351	26	2.0	641	12	AD159337	Ad159337 Wheat ser
279	28	2.0	1041	8	ACC50221	352	26	2.0	646	6	ABQ99078	Abq99078 Human ORF
280	28	2.0	1041	12	ADN04997	353	26	2.0	646	10	ADK58028	Adk58028 Plant DNA
281	28	2.0	1041	13	ADP55492	354	26	2.0	656	10	ADK58028	Adk58028 Plant DNA
282	28	2.0	1041	13	ADP55492	355	26	2.0	718	6	ABQ13576	Abq13576 Oligonuc
283	28	2.0	1119	10	ADB78916	356	26	2.0	718	6	ABQ13576	Abq13576 Oligonuc
284	28	2.0	1119	10	ADB78916	357	26	2.0	753	6	ABQ39707	Abq39707 Oligonuc
285	28	2.0	1119	11	ACL26493	358	26	2.0	753	6	ABQ39707	Abq39707 Oligonuc
286	28	2.0	1161	12	ADN30327	359	26	2.0	764	6	ABQ30109	Abq30109 Oligonuc
287	28	2.0	1161	12	ADN30327	360	26	2.0	764	6	ABQ30109	Abq30109 Oligonuc
288	28	2.0	1161	14	AEA08536	361	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
289	28	2.0	1161	14	AEA08536	362	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
290	28	2.0	1373	3	AA258981	363	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
291	28	2.0	1403	4	AA158073	364	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
292	28	2.0	1403	4	AA158073	365	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
293	28	2.0	1444	4	AA159859	366	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
294	28	2.0	1587	4	ABA09559	367	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
295	28	2.0	1587	4	ABA09559	368	26	2.0	776	6	ABQ17567	Abq17567 Oligonuc
296	28	2.0	1720	14	ADW16415	369	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
297	28	2.0	2000	8	ADA73300	370	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
298	28	2.0	2000	8	ADA73300	371	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
299	28	2.0	2000	8	ADA73300	372	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
300	28	2.0	2000	8	ADA73300	373	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
301	28	2.0	2000	8	ADA73300	374	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
302	28	2.0	2000	8	ADA73300	375	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
303	28	2.0	2000	8	ADA73300	376	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
304	28	2.0	2000	8	ADA73300	377	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
305	28	2.0	2000	8	ADA73300	378	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
306	28	2.0	2000	8	ADA73300	379	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
307	28	2.0	2000	8	ADA73300	380	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
308	28	2.0	2000	8	ADA73300	381	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
309	28	2.0	2000	8	ADA73300	382	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
310	28	2.0	2000	8	ADA73300	383	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc
311	28	2.0	2000	8	ADA73300	384	26	2.0	854	6	ABQ31175	Abq31175 Oligonuc

C 385	2	2.0	1278	14	ABE67635	ABE67635 Rice gene
C 386	26	2.0	1291	6	ABQ39948	ABQ39948 Oligonucle
C 387	26	2.0	1291	6	ABQ39948	ABQ39948 Oligonucle
C 388	26	2.0	1353	5	ABA09728	ABA09728 Human bon
C 389	26	2.0	1393	13	ADT17101	ADT17101 Plant cDN
C 390	26	2.0	1445	14	ADM16421	ADM16421 Eucalyptu
C 391	26	2.0	1449	13	ADU02022	ADU02022 Novel hum
C 392	26	2.0	1464	8	ADH69463	ADH69463 Rice gene
C 393	26	2.0	1479	8	ADA71296	ADA71296 Rice gene
C 394	26	2.0	1493	12	ACH91938	ACH91938 Human gen
C 395	26	2.0	1497	6	ABQ22357	ABQ22357 Oligonucle
C 396	26	2.0	1497	6	ABQ22356	ABQ22356 Oligonucle
C 397	26	2.0	1523	13	ADK63199	ADK63199 Plant full
C 398	26	2.0	1559	13	ADP79328	ADP79328 Human cas
C 399	26	2.0	1559	13	ADP79326	ADP79326 Human cas
C 400	26	2.0	1559	14	ADX07095	ADX07095 Cyclin-de
C 401	26	2.0	1559	14	ABE94287	ABE94287 Human cae
C 402	26	2.0	1615	12	ADQ87148	ADQ87148 Human tum
C 403	26	2.0	1615	13	ADQ84862	ADQ84862 Human tum
C 404	26	2.0	1666	14	ADX07289	ADX07289 Cyclin-de
C 405	26	2.0	1681	14	ADM16693	ADM16693 Eucalyptu
C 406	26	2.0	1714	5	ADM19393	ADM19393 Novel hum
C 407	26	2.0	1716	5	ADM19637	ADM19637 Novel hum
C 408	26	2.0	1719	12	AD119351	AD119351 Wheat sear
C 409	26	2.0	1719	12	AD165936	AD165936 Wheat sear
C 410	26	2.0	1740	2	AAV35446	AAV35446 Rat rSK2
C 411	26	2.0	1742	13	ADXS1777	ADXS1777 Plant full
C 412	26	2.0	1835	11	ADM02866	ADM02866 Human cDN
C 413	26	2.0	2000	8	ADA72576	ADA72576 Rice gene
C 414	26	2.0	2000	11	ACL37458	ACL37458 Rice stre
C 415	26	2.0	2000	11	ACL37395	ACL37395 Rice stre
C 416	26	2.0	2000	11	ACL38938	ACL38938 Rice stre
C 417	26	2.0	2000	11	ACL36748	ACL36748 Rice stre
C 418	26	2.0	2000	11	ACL38031	ACL38031 Rice stre
C 419	26	2.0	2000	11	ACL38778	ACL38778 Rice stre
C 420	26	2.0	2000	12	ADJ41376	ADJ41376 Plant cDN
C 421	26	2.0	2000	12	ADJ40913	ADJ40913 Plant cDN
C 422	26	2.0	2214	13	ADX51086	ADX51086 Plant full
C 423	26	2.0	2210	12	AAJF44644	AAJF44644 Novel pro
C 424	26	2.0	2310	12	ADM129342	ADM129342 Human MMR
C 425	26	2.0	2358	11	ADM02506	ADM02506 Human cDN
C 426	26	2.0	2417	12	ADQ22311	ADQ22311 Human soc
C 427	26	2.0	2632	13	ACN41020	ACN41020 Tumour-as
C 428	26	2.0	2802	13	ADTS45917	ADTS45917 Metastati
C 429	26	2.0	2829	4	AAKS1576	AAKS1576 Human pol
C 430	26	2.0	2832	2	AAV69289	AAV69289 Murine JN
C 431	26	2.0	2835	5	AAKS5260	AAKS5260 Human ova
C 432	26	2.0	2843	5	AAE62269	AAE62269 Human pol
C 433	26	2.0	2853	2	AAV62462	AAV62462 Rat trans
C 434	26	2.0	2993	12	ADQ84014	ADQ84014 Human tum
C 435	26	2.0	3009	13	ACN40429	ACN40429 Tumour-as
C 436	26	2.0	3009	14	ABE044220	ABE044220 Human KSR
C 437	26	2.0	3060	2	AAK39667	AAK39667 Renal can
C 438	26	2.0	3099	6	ABH59914	ABH59914 Novel hum
C 439	26	2.0	3171	4	AAK94415	AAK94415 Human ful
C 440	26	2.0	3171	12	ADL311150	ADL311150 Full leng
C 441	26	2.0	3297	8	AAE91437	AAE91437 DNA encod
C 442	26	2.0	3427	5	ABE63589	ABE63589 Human cDN
C 443	26	2.0	3427	9	ADA24495	ADA

[illegible]







DB 1141 AGTGGGCGGCTCTTCTGTGGAGGGGACCCGGCTCCACACACACATCGCGCCCTTA 1200  
QY 1220 GAGAGCGCAGCCATCTGAGAGCAAGAGATTAACAGAAAGACACCCCTCTTAGGGT 1279  
DB 1201 GAGAGCGCAGCCATCTGTGAGCAAGAGATTAACAGAAAGACACCCCTCTTAGGGT 1260  
QY 1280 CCCCAGGGGGGCGGGGCTGGGGCTGCGTAGGTGAAGAGGCGAG 1321  
DB 1261 CCCCAGGGGGGCGGGGCTGGGGCTGCGTAGGTGAAGAGGCGAG 1302

RESULT 3  
ACN40804  
ID ACN40804 standard; cDNA; 4911 BP.  
ACN40804;  
18-NOV-2004 (first entry)  
Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.  
Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
tumour; diagnosis; cell proliferative disorder; breast cancer;  
colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
central nervous system cancer; bladder cancer; pancreatic cancer;  
cervical cancer; melanoma; leukaemia; hybridisation probe;  
chromosome identification; chromosome mapping; gene mapping;  
gene therapy; cytostatic; gene; ss.

OS Homo sapiens.  
XX WO2004030615-A2.  
XX 15-APR-2004.  
XX 29-SEP-2003; 2003WO-US028547.  
XX 02-OCT-2002; 2002US-0414971P.  
XX (GENTH) GENTHECH INC.  
XX Wu TD, Zhang Z, Zhou Y;  
PI WPI; 2004-347921/32.  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
PS Claim 1; SEQ ID NO 5823; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)  
XX polypeptides, and their related nucleic acids. The TAT polypeptides are  
XX overexpressed in cancer tissues compared to normal tissues, and may thus  
XX serve as effective targets for the diagnosis and treatment of cancer in  
XX mammals. The invention also relates to nucleic acid and polypeptide  
XX sequences at least 80% identical to the TAT nucleic acids and  
XX polypeptides; expression vectors and host cells comprising a TAT nucleic  
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic  
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a  
XX TAT polypeptide; and methods and compositions for the treatment or  
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
XX antibodies, antagonists, binding molecules and compositions are useful  
XX for diagnosing or treating a cell proliferative disorder associated with  
XX increased TAT expression, particularly cancers such as breast cancer,  
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
XX cancer, pancreatic cancer, cervical cancer, cancers of the central  
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
XX used as hybridisation probes, in chromosome and gene mapping, in  
XX chromosome identification and in gene therapy. The present sequence  
XX represents a TAT nucleic acid of the invention

XX SQ Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;  
Query Match 96.5%; Score 1301; DB 13; Length 4911;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AACCCGATCTCTTGAATGATGAGAGAGAGGCGGCGGCGCGCGCGCGAG 80  
DB 1 AACCCGATCTCTTGAATGATGAGAGAGAGAGGCGGCGGCGCGCGCGAG 60  
QY 81 GCGCTCGGCTGGGAGAAAGCTAGCGGAGAGGCTTACGCCCGCGGAGCGCGCCG 140  
DB 61 GCGCTCGGCTGGGAGAAAGCTAGCGGAGAGGCTTACGCCCGCGGAGCGCGCCG 120  
QY 141 TGCAGAGCCATTTTCGAGACGCCACCGCGGGGCACTGCCGACGCCCGGGGCTGG 200  
DB 121 TGCAGAGCCATTTTCGAGACGCCACCGCGGGGCACTGCCGACGCCCGGGGCT 180  
QY 201 GGGAGGCGGGGGGGGGCGAGGGAGCGGCGGCTCCGCACTGAGGCCCGCGGGCG 260  
DB 181 GGGAGGCGGGGGGGGGCGAGGGAGCGGCGGCTCCGCACTGAGGCCCGCGGGCG 240  
QY 261 GAACCTGGCGGCGAGCCCGAGCCCGGAGCCCGGGGCGGCTCCCGCGCGCGCTCC 320  
DB 241 GAACCTGGCGGCGAGCCCGAGCCCGGAGCCCGGGGCGGCTCCCGCGCGCGCTCC 300  
QY 321 TGCATGCGGGGCGCCAGCTCCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 380  
DB 301 TGCATGCGGGGCGCCAGCTCCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 360  
QY 381 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440  
DB 361 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
QY 441 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 500  
DB 421 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
QY 501 TGTTCAGAGCAGTAGAGATCAAGAGCTGAGATTGTTTCAGATCATCATCGTGG 560  
DB 481 TGTTCAGAGCAGTAGAGATCAAGAGCTGAGATTGTTTCAGATCATCATCGTGG 540  
QY 561 TGTATATGTATGT 620  
DB 541 TGTATATGTATGT 600  
QY 621 GGTCTTTCATGACCGGAGACAGCGGCGGAGGAGAGAGATGCTGTCTTCAGAG 680  
DB 601 GGTCTTTCATGACCGGAGACAGCGGCGGAGGAGAGAGATGCTGTCTTCAGAG 660  
QY 681 GATGCTGTGTGCGCTTCGAGAGACAGGTGTCAAGGCAAGTCCCAAGCGCGAGTCT 740  
DB 661 GATGCTGTGTGCGCTTCGAGAGACAGGTGTCAAGGCAAGTCCCAAGCGCGAGTCT 720  
QY 741 AGGCGGCGCTTGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGT 800  
DB 721 AGGCGGCGCTTGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGT 780  
QY 801 TCCACGCGCTTCAGAGCCCACTTACGTTACCTGACAGACGAGATGACCTGCCACCA 860  
DB 781 TCCACGCGCTTCAGAGCCCACTTACGTTACCTGACAGACGAGATGACCTGCCACCA 840  
QY 861 TCTGCTGTGACAGCGGAGAGAGCCCACTTACAGGCGGCGGCGGCGGCGGCGTTC 920  
DB 841 TCTGCTGTGACAGCGGAGAGAGCCCACTTACAGGCGGCGGCGGCGGCGGCGTTC 900  
QY 921 GGGAGCCCGGAGAGAGCTGGAATCTGAATCCGGGAATCGGTGGCGGCAACCCCAAGAA 980  
DB 901 GGGAGCCCGGAGAGAGCTGGAATCTGAATCCGGGAATCGGTGGCGGCAACCCCAAGAA 960  
QY 981 CCATCTGAGACAGTAGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1040

Db 961 CCATCTTCGACGATGACCTGATGATGTCGACGAGCTGCGGCGCCCTGCCCCCAGCA 1020  
Qy 1041 GTACTCTGGGATATGAGCCGACCTGCTACGGCAATGGGGGGCGATGAGGGGGCGCGC 1100  
Db 1021 GTACTCTGGGATATGAGCCGACCTGCTACGGCAATGGGGGGCGATGAGGGGGCGCGC 1080  
Qy 1101 CCACCTACAGGAGGATCTGAGGCACTACCGGGGCTCTCTTCAGAGCAGGAGCA 1160  
Db 1081 CCACCTACAGGAGGATCTACCGGCACTACCGGGGCTCTCTTCAGAGCAGGAGCA 1140  
Qy 1161 GTGGGCGCGCTCTCTCTGAGGAGGACCGGCTTCACACACACATCGCGCCCTAG 1220  
Db 1141 GTGGGCGCGCTCTCTCTGAGGAGGACCGGCTTCACACACACATCGCGCCCTAG 1200  
Qy 1221 AGAGCGGAGGATCTGAGGCAAGAGATTAACAGAAAGACACCCCTCTAGAGGTC 1280  
Db 1201 AGAGCGGAGGATCTGAGGCAAGAGATTAACAGAAAGACACCCCTCTAGAGGTC 1260  
Qy 1281 CCCAGGGGCGCGGCTGAGGCTGCGTAGGTGAAAGGAG 1321  
Db 1261 CCCAGGGGCGCGGCTGAGGCTGCGTAGGTGAAAGGAG 1301

RESULT 4  
ACC49552  
ID ACC49552 standard; cDNA: 4839 BP.  
XX ACC49552;  
AC ACC49552;  
XX 01-JUL-2003 (first entry)  
XX  
DE Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.  
XX  
XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;  
KM Cancer; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003024392-A2.  
PN  
XX  
XX 27-MAR-2003.  
PD  
XX  
XX 11-SEP-2002; 2002WO-US028859.  
PF  
XX  
XX 18-SEP-2001; 2001US-0322268P.  
PR 19-OCT-2001; 2001US-0339227P.  
PR 07-NOV-2001; 2001US-0336827P.  
PR 20-NOV-2001; 2001US-0331906P.  
PR 02-JAN-2002; 2002US-0345444P.  
PR 03-APR-2002; 2002US-0369724P.  
PR 19-AUG-2002; 2002US-0404809P.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Priantz G, Hillan KJ, Philippe HS, Polakis P, Spencer SD,  
PI Williams PM, Wu TD, Zhang Z;  
XX  
XX WPI; 2003-354551/33.  
DR P-PSDB; ABP97234.  
XX  
XX New antibodies against tumor-associated antigenic target polypeptide,  
PT useful for treating or diagnosing tumors or cancers in mammals e.g.  
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell  
PT carcinoma.  
XX  
XX Claim 2; Fig 119; 285pp; English.  
XX  
XX ACC49493 to ACC49552 encode the human tumour-associated antigenic target  
CC (TAT) proteins given in ABP97175 to ABP97234. The present invention  
CC describes an isolated antibody that binds to a polypeptide having at  
CC least 80 & sequence identity to any of the 60 150-800 residue amino acid  
CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking  
CC its associated signal peptide, encoded by any of the 60 2000-3000 base

CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have  
CC cytosolic activity. The antibody can be used for treating or diagnosing  
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast  
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal  
CC cell carcinomas, or thyroid cancer  
XX  
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;  
Query Match 93.0%; Score 1229; DB 8; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 93 GAAAGCTTACGCGAGAGGCTCAGCCCGGCGGAGCGCGCCGCTGCCAGCCATT 152  
Db 1 GAAAGCTTACGCGAGAGGCTCAGCCCGGCGGAGCGCGCCGCTGCCAGCCATT 60  
Qy 153 TTCCGAGCGCACCCCGGGGCACTGCCAGCGCCCGGGGCTGCCAGGGGAGGCGGGG 212  
Db 61 TTCCGAGCGCACCCCGGGGCACTGCCAGCGCCCGGGGCTGCCAGGGGAGGCGGGG 120  
Qy 213 GGGCGCAGGGAGGCGGGTCCCGGCACTAGGCCCGGGGCGCCCGGAACTTGGCGGC 272  
Db 121 GGGCGCAGGGAGGCGGGTCCCGGCACTAGGCCCGGGGCGCCCGGAACTTGGCGGC 180  
Qy 273 GACCCGAGCCCGGAGAGCGGAGCGGCGCTCCCGCGCGCGCTCTGCATGCGGGG 332  
Db 181 GACCCGAGCCCGGAGAGCGGAGCGGCGCTCCCGCGCGCGCTCTGCATGCGGGG 240  
Qy 333 CCCAGCTTCGGGCGCGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 392  
Db 241 CCCAGCTTCGGGCGCGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
Qy 393 GCGCGCGCGCGCGCGCTCCATGACGCGCTTGAATGGGGGTCAACAGACCGCGCGCG 452  
Db 301 GCGCGCGCGCGCGCGCTCCATGACGCGCTTGAATGGGGGTCAACAGACCGCGCGCG 360  
Qy 453 CCGCGGGGAGCCCAATGCTCTCTGCACTGCACTGCACTGCACTGCTTTGTTCCAGACA 512  
Db 361 CCGCGGGGAGCCCAATGCTCTCTGCACTGCACTGCACTGCACTGCTTTGTTCCAGACA 420  
Qy 513 TGGAGATCAGGAGCTGAGTTGTTTCAATCATCATCTGCTGATGATGATGATGATG 572  
Db 421 TGGAGATCAGGAGCTGAGTTGTTTCAATCATCATCTGCTGATGATGATGATGATG 480  
Qy 573 TGGTGTGTGATACGATGCTGCTGCACTGCACTGCACTGCACTGCTGCTGCTGCTG 632  
Db 481 TGGTGTGTGATACGATGCTGCTGCACTGCACTGCACTGCACTGCTGCTGCTGCTG 540  
Qy 633 GCCGCGACAGCGGAGGCGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 692  
Db 541 GCCGCGACAGCGGAGGCGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Qy 693 CTTGAGAGAGCAGTGTCAAGCAAGGATCCAGAGCGGAGGCTTACGCGCCGCTC 752  
Db 601 CTTGAGAGAGCAGTGTCAAGCAAGGATCCAGAGCGGAGGCTTACGCGCCGCTC 660  
Qy 753 GGGCCACCGACCGCTGCGCGGCTGCGCGCTTGGCGGAGCGGCTTCCACGCTTCC 812  
Db 661 GGGCCACCGACCGCTGCGCGGCTGCGCGCTTGGCGGAGCGGCTTCCACGCTTCC 720  
Qy 813 AGCCCACTTACCTGATCTGAGAGAGATGATGATGATGATGATGATGATGATGATG 872  
Db 721 AGCCCACTTACCTGATCTGAGAGAGATGATGATGATGATGATGATGATGATGATG 780  
Qy 873 AGCGGAGAGAGCGCCCACTTACCAAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 932  
Db 781 AGCGGAGAGAGCGCCCACTTACCAAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 933 AGCAGCTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 992  
Db 841 AGCAGCTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 900  
Qy 993 GTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052



QY 813 AGCCACCTATCCGTAACCTGAGACGAGATGCACTTGCCACCCACCATCTCGGTGACG 872  
DB 721 AGCCCACTATCCGTAACCTGAGACGAGATGCACTTGCCACCCACCATCTCGGTGACG 780  
QY 873 ACGGAG 932  
DB 781 ACGGAG 840  
QY 933 AGCAGCTGGAATGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992  
DB 841 AGCAGCTGGAATGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052  
DB 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
QY 1053 TCAG 1112  
DB 961 TCAG 1020  
QY 1113 AGGTGATGAG 1172  
DB 1021 AGGTGATGAG 1080  
QY 1173 CCTTGTGAG 1232  
DB 1081 CCTTGTGAG 1140  
QY 1233 TCTGAG 1292  
DB 1141 TCTGAG 1200  
QY 1293 GGGCTGGGGCTGCTGAGGTGAAAAGGCGAG 1321  
DB 1201 GGGCTGGGGCTGCTGAGGTGAAAAGGCGAG 1229

RESULT 6  
ADP65729  
ID ADP65729 standard; DNA; 4839 BP.

XX AC ADP65729;  
XX DT 12-AUG-2004 (first entry)  
XX DE Human transmembrane, prostate androgen induced RNA (TMEMPR1), DNA.  
XX KW autoimmune disease; arthritis; gene expression analysis; antirheumatic;  
XX KW rheumatoid arthritis; collagen-induced; immunosuppressive; dermatological;  
XX KW antiarthritic; osteopathic; antigout; antiinflammatory; fibrositis;  
XX KW immunomodulatory; lupus; ankylosing spondylitis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
XX KW immune; ds; human.  
XX OS Homo sapiens.  
XX PN WO2003072827-A1.  
XX PD 04-SEP-2003.  
XX PP 31-OCT-2002; 2002WO-US035433.  
XX PR 31-OCT-2001; 2001US-0336220P.  
XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX PI Hirsch R, Thorson SL;  
XX DR WPI; 2003-712740/67.  
XX DR GENBANK; NM\_020182.  
PT Diagnosing and analyzing autoimmune disease using gene expression  
profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
PT gout.  
XX Disclosure; Page; 56pp; English.  
PS  
XX The invention relates to a novel method for diagnosing and analysing  
CC autoimmune disease or arthritides. The method comprises obtaining a  
CC patient sample containing mRNA, analysing gene expression using the mRNA  
CC that results in a gene expression signature of the mRNA, and using that  
CC gene expression signature to diagnose or analyse the autoimmune disease  
CC or arthritides in the patient, where gene expression of at least 60% of  
CC the genes correlates with that of the gene signature. The invention  
CC further comprises a treatment of rheumatoid arthritis; identification of  
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with collagen-  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritides, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This polynucleotide  
CC represents a DNA sequence relating to the genes used in the analysis and  
CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
CC not shown in the specification. It has been supplied in an electronic  
CC format from WIPO.  
XX  
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other:  
Query Match 93.0%; Score 1229; DB 11; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 93 GGAAAGCTAAGCGAG 152  
DB 1 GGAAAGCTAAGCGAG 60  
QY 153 TTCCGAG 212  
DB 61 TTCCGAG 120  
QY 213 GGGGAG 272  
DB 121 GGGGAG 180  
QY 273 GAGCCGAG 332  
DB 181 GAGCCGAG 240  
QY 333 CCCAG 392  
DB 241 CCCAG 300  
QY 393 GCGGAG 452  
DB 301 GCGGAG 360  
QY 453 CCGGAG 512  
DB 361 CCGGAG 420  
QY 513 TGAGATCAG 572  
DB 421 TGAGATCAG 480  
QY 573 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632  
DB 481 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540









Db 181 GACCCGAGCCGCGGAGCCGCGGCGCTCCCGCGCGCGCGCTCCGATGCGGAGC 240  
 Qy 333 CCCAGCTCCGCGGCGCGGCGCGAGCCCCCGCGCGCGCGCGCGCGCGCGC 392  
 Db 241 CCCAGCTCCGCGGCGCGGCGCGAGCCCCCGCGCGCGCGCGCGCGCGC 300  
 Qy 333 GC 452  
 Db 301 GC 360  
 Qy 453 CGC 512  
 Db 361 CGC 420  
 Qy 513 TGGAGATCA CGAGCTGAGTTGTTGATCATCATCATCATCATCATCATCATCATCA 572  
 Db 421 TGGAGATCA CGAGCTGAGTTGTTGATCATCATCATCATCATCATCATCATCATCA 480  
 Qy 573 TGGAGATCA CGAGCTGAGTTGTTGATCATCATCATCATCATCATCATCATCATCA 632  
 Db 481 TGGAGATCA CGAGCTGAGTTGTTGATCATCATCATCATCATCATCATCATCATCA 540  
 Qy 633 GC 692  
 Db 541 GC 600  
 Qy 693 CCTCGGAGAGCA GAGTGTGAGGCA GGAATCCAGAGCGCGAGTCTA CGCGCGCGCTC 752  
 Db 601 CCTCGGAGAGCA GAGTGTGAGGCA GGAATCCAGAGCGCGAGTCTA CGCGCGCGCTC 660  
 Qy 753 GC 812  
 Db 661 GC 720  
 Qy 813 AGCCCACTATCGATGCTGAGCGAGCGAGATGAGCTGCGACCACTCTGCTGTGAG 872  
 Db 721 AGCCCACTATCGATGCTGAGCGAGCGAGATGAGCTGCGACCACTCTGCTGTGAG 780  
 Qy 873 AGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 932  
 Db 781 AGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 840  
 Qy 933 AGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 992  
 Db 841 AGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 900  
 Qy 993 GGTGAGCTGATGATGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1052  
 Db 901 GGTGAGCTGATGATGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 960  
 Qy 1053 TGAGCGCGAGCTGCTACGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGC 1112  
 Db 961 TGAGCGCGAGCTGCTACGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGC 1020  
 Qy 1113 AGGTGATGCGGCACTAACCAGGCTCTCTTCCAGACA GAGAGAGATGCGCGCGCT 1172  
 Db 1021 AGGTGATGCGGCACTAACCAGGCTCTCTTCCAGACA GAGAGAGATGCGCGCGCT 1080  
 Qy 1173 CCTTGTGAGAGGAGCGCGCGCTCAACA GAGAGATGCGCGCGCGCGCGCGCGC 1232  
 Db 1081 CCTTGTGAGAGGAGCGCGCGCTCAACA GAGAGATGCGCGCGCGCGCGCGCGC 1140  
 Qy 1233 TCTGAGCAAGAGAGATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292  
 Db 1141 TCTGAGCAAGAGAGATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
 Qy 1293 GGGCTGGGGCTGCGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321  
 Db 1201 GGGCTGGGGCTGCGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1229

RESULT 9  
 ADR66778

ID ADR66778 standard; DNA; 4839 BP.  
 AC ADR66778;  
 DT 02-DEC-2004 (first entry)  
 DE Human prostatic carcinoma derived DNA SEQ ID 71 #4.  
 XX human; cyrostatic; diagnosis; prostatic cancer;  
 KM differential expression analysis; ds.  
 XX Homo sapiens.  
 OS WO2004076614-A2.  
 PN 10-SEP-2004.  
 PD 22-FEB-2004; 2004WO-DE000433.  
 PF 27-FEB-2003; 2003DE-01009985.  
 PR 14-MAY-2003; 2003DE-01022134.  
 XX (HINZ//) HINZMANN B.  
 PA (DAHL//) DAHL E.  
 PA (ROSE//) ROSENTHAL A.  
 PA (HERM//) HERMANN K.  
 PA (PILAU//) PILARSKY C.  
 XX Hinmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T,  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinemann H, Roepcke S;  
 PI Xinhong L, Staub E,  
 DR WPI; 2004-653386/63.  
 PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 PS Claim 1; Page 1447; 1607pp; German.  
 XX This invention describes novel cyrostatic polynucleotide and polypeptide  
 CC sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection  
 CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumor cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular  
 CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays,  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;  
 CC biotinylated second antibody; streptavidin-conjugated horseradish  
 CC peroxidase and then diaminobenzidine as colour former (brown). The  
 CC samples were counterstained with hemalum (blue). Malignant cells stained  
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
 CC lymph node metastases were also stained. ADR6505-ADR6694 represent the  
 CC polynucleotide and polypeptide sequences used in the method of the  
 CC invention.  
 SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;



Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGCCGCTGCGAGCCCAATT 152  
Db 1 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGCCGCTGCGAGCCCAATT 60

QY 153 TTCCGAGCGCACTCCGCGGAGCTGCGCAAGCCCGCGGAGCTGCGAGGAGGCGCGG 212  
Db 61 TTCCGAGCGCACTCCGCGGAGCTGCGCAAGCCCGCGGAGCTGCGAGGAGGCGCGG 120

QY 213 GGGGCGAGCGGAGCGGCTCCGCGGAGCTGAGCCCGCGGAGCGCCCGGAAAATTGCGCGG 272  
Db 121 GGGGCGAGCGGAGCGGCTCCGCGGAGCTGAGCCCGCGGAGCGCCCGGAAAATTGCGCGG 180

QY 273 GACCCGAGCGCGGAGCGGAGCGGCGGCTCCCGCGGAGCGGCGCTCTGAGCGGAGG 332  
Db 181 GACCCGAGCGCGGAGCGGAGCGGCGGCTCCCGCGGAGCGGCGCTCTGAGCGGAGG 240

QY 333 CCGAGCTCCGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392  
Db 241 CCGAGCTCCGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300

QY 393 GCGCGCGCGCGCGCGGCTCCAGCAAGCGGCTGAGTGAAGGAGCGGCGGCGGCGG 452  
Db 301 GCGCGCGCGCGCGGCTCCAGCAAGCGGCTGAGTGAAGGAGCGGCGGCGGCGGCGG 360

QY 453 CCGCGCGGAGCGGAGCTGCTCTGCGAGCGTGAAGCGCTCTTGTTCAGAGCA 512  
Db 361 CCGCGCGGAGCGGAGCTGCTCTGCGAGCGTGAAGCGCTCTTGTTCAGAGCA 420

QY 513 TGGAGATCAAGGAGCTGAGATTGTTTCAAGATCATCATCGTGGTGTGATGATGATGA 572  
Db 421 TGGAGATCAAGGAGCTGAGATTGTTTCAAGATCATCATCGTGGTGTGATGATGATGA 480

QY 573 TGGTGGTGTGATCAAGTGGCTGAGCGCACTAAGGCTGAGCGGCTTCTCATCA 632  
Db 481 TGGTGGTGTGATCAAGTGGCTGAGCGCACTAAGGCTGAGCGGCTTCTCATCA 540

QY 633 GCGGCGAGCGGAGCGGAGGAGAGAGATGCTGCTCAGAGAGATGCTGTGAGC 692  
Db 541 GCGGCGAGCGGAGCGGAGGAGAGAGATGCTGCTCAGAGAGATGCTGTGAGC 600

QY 693 CCGGAGAGCAAGTGTGAGGCAAGAAATCCAGAGCGGAGCTTACGCGCGCTC 752  
Db 601 CCGGAGAGCAAGTGTGAGGCAAGAAATCCAGAGCGGAGCTTACGCGCGCTC 660

QY 753 GCGGCGAGCGGCTGCGGCTGCGGCTTGGCCAGGAGGAGGCTTCCACCGCTCC 812  
Db 661 GCGGCGAGCGGCTGCGGCTGCGGCTTGGCCAGGAGGAGGCTTCCACCGCTCC 720

QY 813 AGCCCACTATCGGAGCTGAGCAAGATGAGCTGCGCACTTCCACATCTGCTGAG 872  
Db 721 AGCCCACTATCGGAGCTGAGCAAGATGAGCTGCGCACTTCCACATCTGCTGAG 780

QY 873 AGGAGGAGGAGCGGAGCGGCTTACAGAGGCGCTTGAAGCTTCCAGGCTTCCAGG 932  
Db 781 AGGAGGAGGAGCGGAGCGGCTTACAGAGGCGCTTGAAGCTTCCAGGCTTCCAGG 840

QY 933 AGGAGCTGAGAGCTGAGCGGAGGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 992  
Db 841 AGGAGCTGAGAGCTGAGCGGAGGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 900

QY 993 GTGAGCTGAGTGAAGTGAAGGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1052  
Db 901 GTGAGCTGAGTGAAGTGAAGGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 960

QY 1053 TTAGCGGCAAGTGTCTTACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1112  
Db 961 TTAGCGGCAAGTGTCTTACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1020

QY 1113 AGGTATGCGGCACTACCGGAGGCTCTCTTCCAGAGCAAGAGAGCAATGAGCGGCGCT 1172

Db 1021 AGGTATGCGGCACTACCGGAGGCTCTCTTCCAGAGCAAGAGAGCAATGAGCGGCGCT 1080  
QY 1173 CCGTGTGAGGAGGAGCGGAGCTCCAGCAAGCAATCGGCGGCGCTTGAAGCGGAGCGCA 1232  
Db 1081 CCGTGTGAGGAGGAGCGGAGCTCCAGCAAGCAATCGGCGGCGCTTGAAGCGGAGCGCA 1140

QY 1233 TCTGAGCAAGAGAGATTAACAGAAAGAGACCGCTCTTGAAGGTCCTCCAGGAGGAGG 1292  
Db 1141 TCTGAGCAAGAGAGATTAACAGAAAGAGACCGCTCTTGAAGGTCCTCCAGGAGGAGG 1200

QY 1293 GGGCTGAGGAGCTGCTAGGTGAAAAGCGAG 1321  
Db 1201 GGGCTGAGGAGCTGCTAGGTGAAAAGCGAG 1229

RESULT 11  
ADM43368  
ID ADM43368 standard; DNA; 4839 BP.  
XX  
AC ADM43368;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Prostate cancer related gene, SEQ ID 166.  
XX  
KM Cyrostatic; Gene Therapy; Prostate tumor; prostatic cancer; diagnosis;  
KM ds; gene.  
XX  
OS Homo sapiens.  
XX  
PN MO2004113571-A2.  
XX  
PD 29-DEC-2004.  
XX  
PF 25-JUN-2004; 2004WO-IB002394.  
XX  
PR 26-JUN-2003; 2003US-0482595P.  
XX  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
XX  
PI Einstein R, McGowan KM, Pando MP;  
XX  
DR WPI, 2005-057996/06.  
XX  
CC The present invention relates to novel nucleic acid sequences that are  
CC expressed by human prostate cancer cells. The nucleic acid sequences or  
CC the encoded proteins are useful as targets for treating, preventing  
CC and/or diagnosing cancers, particularly prostate cancer. The present  
CC sequence is one such nucleic acid of the invention.  
XX  
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 14; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGCCGCTGCGAGCCCAATT 152  
Db 1 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGCCGCTGCGAGCCCAATT 60

QY 153 TTCCGAGCGCACTCCGCGGAGCTGCGCAAGCCCGCGGAGCTGCGAGGAGGCGCGG 212  
Db 61 TTCCGAGCGCACTCCGCGGAGCTGCGCAAGCCCGCGGAGCTGCGAGGAGGCGCGG 120

QY 213 GGGGCGAGCGGAGCGGCTCCGCGGAGCTGAGCCCGCGGAGCGCCCGGAAAATTGCGCGG 272  
Db 121 GGGGCGAGCGGAGCGGCTCCGCGGAGCTGAGCCCGCGGAGCGCCCGGAAAATTGCGCGG 180

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QY 273 GACCCGAGCCCGGCGAGCCGCGCGCTCCCGCCGCGCTCTCTGATGCGGGGC 332
DB 181 GACCCGAGCCCGGCGAGCCGCGCGCTCCCGCCGCGCGCTCTCTGATGCGGGGC 240
QY 333 CCCAGCTCGGGGCGCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
DB 241 CCCAGCTCGGGGCGCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 393 GCCCGCGCGCGCGCGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 452
DB 301 GCCCGCGCGCGCGCGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 360
QY 453 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 512
DB 361 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 513 TGGAGATCAGGAGCTGAGGTTGTTGATGATGATGATGATGATGATGATGATGAT 572
DB 421 TGGAGATCAGGAGCTGAGGTTGTTGATGATGATGATGATGATGATGATGATGAT 480
QY 573 TGGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632
DB 481 TGGTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 633 GCCCGGCAAGCCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 692
DB 541 GCCCGGCAAGCCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 693 CCTGGAGAGGCAATGTCAGGCGCAAGGATCCGAGAGCGGAGGCTTACGCGCGCT 752
DB 601 CCTGGAGAGGCAATGTCAGGCGCAAGGATCCGAGAGCGGAGGCTTACGCGCGCT 660
QY 753 GGGCCGACGAGCCGCTGCGCGCTGCGCGCTTCCGCGAGCGGAGGCTTCCAGCGCT 812
DB 661 GGGCCGACGAGCCGCTGCGCGCTGCGCGCTTCCGCGAGCGGAGGCTTCCAGCGCT 720
QY 813 AGCCCACTATTCCTGACTGTCAGCAAGATGATGATGATGATGATGATGATGAT 872
DB 721 AGCCCACTATTCCTGACTGTCAGCAAGATGATGATGATGATGATGATGATGAT 780
QY 873 AGCGGAGAGAGCGCCGACCTTACGAGGCGCGCTGACCTTCCAGGCTTCCGAGCG 932
DB 781 AGCGGAGAGAGCGCCGACCTTACGAGGCGCGCTTCCAGGCTTCCGAGCGCGCG 840
QY 933 AGCAGCTGGAATCTGAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 992
DB 841 AGCAGCTGGAATCTGAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052
DB 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
QY 1053 TGAAGGCGACGCTGACGCGGAGCGGCGGAGGAGGCGCGCGCGCGCGCGCGCG 1112
DB 961 TGAAGGCGACGCTGACGCGGAGCGGCGGAGGAGGCGCGCGCGCGCGCGCGCG 1020
QY 1113 AGGTATGCGGCACTAACCGGGGTCTCTTCCAGACCAAGCAGAGCAGTGGGCGGCT 1172
DB 1021 AGGTATGCGGCACTAACCGGGGTCTCTTCCAGACCAAGCAGAGCAGTGGGCGGCT 1080
QY 1173 CTTTGTGAGAGGAGCGCGGCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1232
DB 1081 CTTTGTGAGAGGAGCGCGGCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1140
QY 1233 TTTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1292
DB 1141 TTTTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1200
QY 1293 GGGGCTGGGGCTGCTAGTGAAGAGAG 1321
DB 1201 GGGGCTGGGGCTGCTAGTGAAGAGAG 1229

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RESULT 12
AD37326 standard; DNA; 1383 BP.
ID AD37326
XX
AC AD37326;
XX
DT 18-DEC-2003 (first entry)
XX
DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.
XX
KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischemic disorder; Antinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiac; Gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN W02003048202-A2.
XX
PD 12-JUN-2003.
XX
PF 03-DEC-2002; 2002MO-JP012644.
XX
PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-035829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX
PA (ASAH ) ASAH KASEI KK.
XX
PI Matsuda A, Muramatsu S;
XX
WP1: 2003-505282/47.
DR P-PSDB; AD37327.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers, or
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 4; SEQ ID NO 159; 938bp; English.
XX
CC The present invention relates to novel proteins and their coding
CC sequences (AD37168-AD37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischemic disorders.
XX
SQ Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;
Query Match 89.2%; Score 1178; DB 10; Length 1383;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 93 GGAAGCTAGGCGGAGAGGCTCAGCCCGGCGGAGCGCGCGCGCGCGCGCGCGCG 152
DB 1 GGAAGCTAGGCGGAGAGGCTCAGCCCGGCGGAGCGCGCGCGCGCGCGCGCGCGCG 60
QY 153 TTCCGAGACGCAACCGCGCGGCACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 212
DB 61 TTCCGAGACGCAACCGCGGCACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 213 GGGGCGAGCGGAGCGGCTCCCGGCACTGAGCGCGCGCGCGCGCGCGCGCGCGCG 272
DB 121 GGGGCGAGCGGAGCGGCTCCCGGCACTGAGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 273 GACCCGAGCCCGGCGAGCCGCGGCGCGCTTCCCGCGCGCGCGCTTCTGATGCGGGGC 332
DB 181 GACCCGAGCCCGGCGAGCCGCGGCGCGCTTCCCGCGCGCGCGCTTCTGATGCGGGGC 240

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OY	333	CCGAGCTCCGGGAGCCCGAGCCGAGACCCCCCGGCGCCGCCAGAGCCCGCGCGCCGCG	392
Db	241	CCGAGCTCCGGGAGCCCGAGCCGAGACCCCCCGGCGCCGCCAGAGCCCGCGCGCCGCG	300
OY	393	GCCGCGCCGCGCGCCGCTGCATGCAACCGCTTGATGAGGAGTCAACAGCAGCCGCGCGCG	452
Db	301	GCCGCGCCGCGCGCCGCTGCATGCAACCGCTTGATGAGGAGTCAACAGCAGCCGCGCGCG	360
OY	453	CCGCGCGGAGACCCCAATGTCCTCCGACAGTGCACATGCAAAACGCTCTTGTCAGAGCA	512
Db	361	CCGCGCGGAGACCCCAATGTCCTCCGACAGTGCACATGCAAAACGCTCTTGTCAGAGCA	420
OY	513	TGAGATCACGAGACTGGAGTTTGTTCAGATCATCATCATCTGCTGATGATGATGATG	572
Db	421	TGAGATCACGAGACTGGAGTTTGTTCAGATCATCATCATCTGCTGATGATGATGATG	480
OY	573	TGCTGTGTGTATCACTGCTGCTGACCACTACAAAGCTGTCTGACCGTCTCTATCA	632
Db	481	TGCTGTGTGTATCACTGCTGCTGACCACTACAAAGCTGTCTGACCGTCTCTATCA	540
OY	633	GCCGCGACAGCAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	692
Db	541	GCCGCGACAGCAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	600
OY	693	CCTCGAGAGACAGAGTGTCAAGGCAACGGAATCCAGAGCCGAGCTTACGCGCCGCTC	752
Db	601	CCTCGAGAGAGACAGAGTGTCAAGGCAACGGAATCCAGAGCCGAGCTTACGCGCCGCTC	660
OY	753	GAGCCACCGACCGCTGCGCTGCCGCTTGGCCCTTGCCCAAGCGGAGAGCGCTTCCAGCTTCC	812
Db	661	GAGCCACCGACCGCTGCGCTGCCGCTTGGCCCTTGCCCAAGCGGAGAGCGCTTCCAGCTTCC	720
OY	813	AGCCCACTTATCCGATACCTGACAGCAGAGATCGACTGACCTGACCCAGCATCTGCTGAC	872
Db	721	AGCCCACTTATCCGATACCTGACAGCAGAGATCGACTGACCTGACCCAGCATCTGCTGAC	780
OY	873	ACGGGAGAGAGCCCGCCACCTTACAGAGGCGCCCTTGACCTTCAGCTTGGAGCCCGAGC	932
Db	781	ACGGGAGAGAGCCCGCCACCTTACAGAGGCGCCCTTGACCTTCAGCTTGGAGCCCGAGC	840
OY	933	AGCAGCTGGAATCTGAACCGGGAGATCGGTGCGCGCACCCCGAAACAGAACATCTTGACA	992
Db	841	AGCAGCTGGAATCTGAACCGGGAGATCGGTGCGCGCACCCCGAAACAGAACATCTTGACA	900
OY	993	GTGACCTGATGATGTATGTGTCAGAGCTGAGGCGGCGCCCTGCGCCAGCAGTAACTCGGACA	1052
Db	901	GTGACCTGATGATGTATGTGTCAGAGCTGAGGCGGCGCCCTGCGCCAGCAGTAACTCGGACA	960
OY	1053	TCAGGCGCAACGTGCTTACGAGCGAGCGGCGGAGCGAGTGAAGGAGCGCGCGCCCACTTACAGCG	1112
Db	961	TCAGGCGCAACGTGCTTACGAGCGAGCGGCGGAGCGAGTGAAGGAGCGCGCGCCCACTTACAGCG	1020
OY	1113	AGGTCATGAGGCACATACCCGGGGGTCTCTCTTCAGACACAGAGAGAGAGTGGGCGCGCTT	1172
Db	1021	AGGTCATGAGGCACATACCCGGGGGTCTCTCTTCAGACACAGAGAGAGAGTGGGCGCGCTT	1080
OY	1173	CCCTGCTGAGAGGAGACCGGCGTCTCAACAACAATGCGCGCCCTTACAGAGCGCAAGCA	1232
Db	1081	CCCTGCTGAGAGGAGACCGGCGTCTCAACAACAATGCGCGCCCTTACAGAGCGCAAGCA	1140
OY	1233	TCGTGAGCAAAAGAGAGAGATTAACAAGAAAGACACCTCTCTTAGGGTCCCCAGGGGGGCC	1292
Db	1141	TCGTGAGCAAAAGAGAGAGATTAACAAGAAAGACACCTCTCTTAGGGTCCCCAGGGGGGCC	1200
OY	1293	GAGGCTGGGGCTGCGTAGGTGAAGAAAGCAG	1321
Db	1201	GAGGCTGGGGCTGCGTAGGTGAAGAAAGCAG	1229

RESULT 13  
ADX97454  
ID . ADX97454 standard; DNA; 4519 BP.  
XX

AC	ADX97454;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	Pancreatic cancer associated human protein encoding DNA, SEQ ID 2.
XX	
KW	pancreas tumor; cytostatic; gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	EPI471075-A2.
PD	
XX	
PD	27-OCT-2004.
XX	
PF	31-MAR-2004; 2004EP-00090124.
XX	
PR	31-MAR-2003; 2003DE-01015834.
XX	
PA	(HINZ/) HINZMANN B.
PA	(ROSE/) ROSENTHAL A.
PA	(PLIA/) PILARSKY C.
PA	(DAHL/) DAHL E.
PA	(SPEC/) SPECHT T.
PA	(LICH/) LICHTNER R.
XX	
PI	Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemendorf T,
PI	Lichtner R, Staud E, Roepcke S, Li X;
DR	WPI; 2004-768082/76.
DR	P-PsDB; ADX97525.
XX	
PT	New nucleic acid differentially expressed in pancreatic tumor tissue, for
PT	use as diagnostic agents and in screening for therapeutic agents.
XX	
PS	Claim 1; SEQ ID NO 2; 28pp; German.
CC	The invention relates to a novel human nucleic acid sequence of the
CC	pancreas and its encoded protein. The invention further comprises:
CC	proteins and peptides, preferably isolated, that contain a sequence
CC	encoded by the novel nucleic acid; and methods for diagnosis and
CC	treatment of pancreatic cancer, using a substance that inhibits or binds
CC	to the protein or its DNA, including: an antisense oligonucleotide, short
CC	interfering RNA or ribozyme directed against the pancreatic protein, an
CC	organic molecule, particularly having a molecular weight below 5000,
CC	especially 300, that binds to the pancreatic DNA, an aptamer or
CC	(monoclonal) antibody, preferably human or humanized, that binds to the
CC	pancreatic DNA, or an anti-idiotypic antibody raised against the
CC	monoclonal antibody, any of which may be derivatized with a reporter
CC	group, cytotoxic compound, immunostimulant and/or radiolotope. The novel
CC	human pancreatic proteins and their encoding DNA have cytosolic
CC	activity. The novel sequences are useful for inhibiting transcription
CC	and/or expression of genes and proteins associated with pancreatic
CC	cancer. This polynucleotide sequence represents the DNA encoding one of
CC	the novel human pancreatic proteins of the invention. Note: This sequence
CC	is not shown in the specification, it has been electronically downloaded
CC	from a DVD-ROM provided with this specification by the European Patent
CC	Office.
XX	
SQ	Sequence 4519 BP; 1074 A; 1162 C; 1169 G; 1114 T; 0 U; 0 Other;
Query Match	68.8%; Score 909; DB 13; Length 4519;
Best Local Similarity	100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0
Matches 909; Conservative	0;
Dbl	413 ATGCACCGCTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGGAGCCCATATGTC 472       1 ATGCACCGCTTGATTGGGGGTCAACAGCACCGCGCGCGCGCGGAGCCCATATGTC 60       473 TCCTCAGCGTGAAGTCAAAACGCTCTTTGTTCCAGAGCATGGAATCAAGAGCTGGAG 532       Db 61 TCCTCAGCGTGAAGTCAAAACGCTCTTTGTTCCAGAGCATGGAATCAAGAGCTGGAG 120       533 TTGTGTCAGATCATCATCATCTGTGGTAGATGAGTGTGTGTATCAAGTGC 592 





[illegible]

RESULT	15
ABK92120	
ID	ABK92120 standard; DNA; 1140 BP.
XX	
AC	ABK92120;
XX	
D7	15-AUG-2002 (first entry)
XX	
DE	Prostate cancer-associated DNA sequence #6.
XX	
KM	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW	gene therapy; gene; ds.
XX	
OS	Mammalia.
XX	
PN	WO200230268-A2.
XX	
PD	18-APR-2002.
XX	

PF	12-OCT-2001; 2001WO-US032045.
XX	13-OCT-2000; 2000US-00687576.
PR	08-DEC-2000; 2000US-00733288.
PR	08-DEC-2000; 2000US-00733742.
PR	16-JAN-2001; 2001US-0263957P.
PR	16-MAR-2001; 2001US-0276791P.
PR	16-MAR-2001; 2001US-0276888P.
PR	06-APR-2001; 2001US-0281922P.
PR	24-APR-2001; 2001US-0286214P.
PR	30-APR-2001; 2001US-00847046.
PR	04-MAY-2001; 2001US-0288589P.
XX	
PA	(EOSB-) EOS BIOTECHNOLOGY INC.
XX	
PI	Glen KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX	
DR	WPI; 2002-471335/50.
DR	P-PSDB; ABG61805.
XX	
PT	Detecting a prostate cancer-associated transcript in a patient,
PT	useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT	by determining if prostate cancer-associated genes are expressed in a
PT	prostate tissue.
PS	Claim 22; Page 305; 436pp; English.
XX	
XX	The present invention relates to methods of detecting a prostate cancer-
CC	associated transcript in a cell from a patient. The method comprises
CC	contacting a biological sample from the patient with prostate cancer-
CC	associated polynucleotides (designated PC genes) that selectively
CC	hybridize to a sequence that is at least 80% identical to them. The
CC	prostate cancer-associated polynucleotide sequences are differentially
CC	expressed in prostate tumour tissue or in prostate cancer and are derived
CC	from the tissues of various organisms such as humans or other mammals
CC	(e.g. mice, sheep and dogs). The methods of the invention are useful for
CC	diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC	associated genes are useful for diagnosing or treating prostate cancer,
CC	as well as for identifying modulators of prostate cancer or agents that
CC	inhibit prostate cancer. The nucleic acid sequences are particularly
CC	useful in gene therapy, as a vaccine or in antisense applications.
CC	ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC	sequences
XX	
XX	Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;
SQ	
Query Match	60.6%; Score 800; DB 6; Length 1140;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	800; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	522 CGAAGCTGAGATTGTCAGATCATCATCGTGTGTGTGATGTGATGTGATGTG 581
DB	100 CGAAGCTGAGATTGTCAGATCATCATCGTGTGTGTGATGTGATGTGATGTG 159
QY	522 TGATACGTGCTGCTGAGACCACTACAGCTGTCTGACAGCTCTTTCATACGGCGGACA 641
DB	160 TGATACGTGCTGCTGAGACCACTACAGCTGTCTGACAGCTCTTTCATACGGCGGACA 219
QY	642 GCGAGGGGCGAGAGAGAGATGCGCTGCTCAGAAAGATGCGTGTGGCCCTCGAGAGA 701
DB	220 GCGAGGGGCGAGAGAGATGCGCTGCTCAGAAAGATGCGTGTGGCCCTCGAGAGA 279
QY	702 GCACAGTGTACGGCAACGGAATCCAGAGCCGACAGTCTACGCCCCGCTCGGACCA 761
DB	280 GCACAGTGTACGGCAACGGAATCCAGAGCCGACAGTCTACGCCCCGCTCGGACCA 339
QY	762 ACCGCTTGCGCTGCGCCCTTCCAGCGGAGAGCGCTTCCACCGCTTTCAGGCCACT 821
DB	340 ACCGCTTGCGCTGCGCCCTTCCAGCGGAGAGCGCTTCCACCGCTTTCAGGCCACT 399
QY	822 ATCCGTAATCGTAGACAGAGATGACCTGACCAACCAACCATTCGCTGTACAGCGGAGAG 881
DB	400 ATCCGTAATCGTAGACAGAGATGACCTGACCAACCAACCATTCGCTGTACAGCGGAGAG 459











DB 280 GCACAGTCTCAGGCAACGGAATCCAGACCGGAGGTCTAGCCCGCTGCGCCACCG 339  
QY 762 ACCGCTGAGCGGTGCGCCCTTCCGCGAGCGGAGCGCTTCCAGCCGCTTCCAGCCACT 821  
DB 340 ACCGCTGAGCGGTGCGCCCTTCCGCGAGCGGAGCGCTTCCAGCCGCTTCCAGCCACT 399  
QY 822 ATCCGTACTCTGAGACGAGATCCGACCTGCGACCCACATCTGCTGTCAGACGGGAGG 881  
DB 400 ATCCGTACTCTGAGACGAGATCCGACCTGCGACCCACATCTGCTGTCAGACGGGAGG 459  
QY 882 AGCCCCCACTTACCGAGGCGCCCTTCCAGCCCTTCCAGCTTCCAGGAGCGAGCTGG 941  
DB 460 AGCCCCCACTTACCGAGGCGCCCTTCCAGCCCTTCCAGCTTCCAGGAGCGAGCTGG 519  
QY 942 AACTGAAACCGGAGGTGCGTGGCGGACCCCGCAACCAACATCTTCCAGCTGACTGA 1001  
DB 520 AACTGAAACCGGAGGTGCGTGGCGGACCCCGCAACCAACATCTTCCAGCTGACTGA 579  
QY 1002 TGGATAGTCCAGGCTGCGGCGGCGCCCTGCGCGAGAGTAACTCGGGCATCGCGGCA 1061  
DB 580 TGGATAGTCCAGGCTGCGGCGGCGCCCTGCGCGAGAGTAACTCGGGCATCGCGGCA 639  
QY 1062 CGTGTCTACGCGAGCGGCGGCGCATGAGAGGCGCGCCCGCACTTACAGCGAGCTCATCG 1121  
DB 640 CGTGTCTACGCGAGCGGCGGCGCATGAGAGGCGCGCCCGCACTTACAGCGAGCTCATCG 699  
QY 1122 GCCACTTACCGGCGGCTCTCTCTTCCAGCACACAGAGAGAGAGTGGCGCGCTCTTCTGG 1181  
DB 700 GCCACTTACCGGCGGCTCTCTCTTCCAGCACACAGAGAGAGAGTGGCGCGCTCTTCTGG 759  
QY 1182 AGGGGACCGGCTCCACACACACATCGCGCCCTTGAAGAGCGGACCATCTGGAGCA 1241  
DB 760 AGGGGACCGGCTCCACACACACATCGCGCCCTTGAAGAGCGGACCATCTGGAGCA 819  
QY 1242 AAGAGAGGATTAACAGAAAGAGACACCTCTCTAGAGTCCCGAGGCGGCGCTGGG 1301  
DB 820 AAGAGAGGATTAACAGAAAGAGACACCTCTCTAGAGTCCCGAGGCGGCGCTGGG 879  
QY 1302 CTGCGTAGTGAAGAGCGAG 1321  
DB 880 CTGCGTAGTGAAGAGCGAG 899

RESULT 21  
ADL83313 standard; cDNA; 4527 BP.  
ID ADL83313;  
AC ADL83313;  
XX 20-MAY-2004 (first entry)  
DT XX  
XX 20-MAY-2004 (first entry)  
DE Human androgen responsive prostate specific nucleic acid, ARP2.  
XX Human; ss; gene; androgen responsive prostate specific; ARP2;  
KM prostate cancer; prostate pathology; benign prostatic hyperplasia;  
KM prostatic; prostatic neoplasm.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 96..854  
FT /\*tag= a  
FT /product= "ARP2"  
FT misc\_feature 1128..4509  
FT /\*tag= b  
FT /note= "Claimed in claim 10"

US2003166520-A1.  
04-SEP-2003.  
28-MAR-2001; 2001US-00821812.

XX 28-MAR-2001; 2001US-00821812.  
PR (LINE/) LIN B.  
XX LIn B;  
XX WPI: 2003-898096/82.  
DR P-PSDB: ADL83314.  
XX New substantially pure androgen responsive prostate specific nucleic acid  
PT molecules and polypeptides, useful for diagnosing, preventing and  
PT treating prostate cancer or other prostatic pathologies, e.g.  
PT prostatics.  
XX  
PS Claim 9; SEQ ID NO 2; 43pp; English.  
XX  
XX The invention relates to a substantially pure androgen responsive  
CC prostate specific (ARP) nucleic acid molecule selected from ARP1-ARPs  
CC (appearing as ADL83312, ADL83313, ADL83315, ADL83317 and ADL83319. Also  
CC included are methods of diagnosing or predicting susceptibility to a  
CC prostate neoplastic condition in an individual, methods for treating or  
CC reducing the severity of a prostate neoplastic condition in an  
CC individual, a substantially pure ARP3, ARP4 or ARP5 polypeptide (or their  
CC fragments, encoded by the above ARP3, ARP4 or ARP5 nucleic acid molecule,  
CC respectively) and a binding agent comprising a molecule that selectively  
CC binds the above ARP3, ARP4 or ARP5 polypeptide. The nucleic acid  
CC molecules and polypeptides are useful in diagnosing, preventing and  
CC treating prostate cancer or other prostate pathologies such as benign  
CC prostatic hyperplasia or prostatics. The nucleic acid molecules are used  
CC as hybridisation probes in various diagnostic procedures. The present  
CC sequence is the ARP2 cDNA.  
XX  
SQ Sequence 4527 BP; 1089 A; 1149 C; 1175 G; 1113 T; 0 U; 1 Other;  
Query Match 60.6%; Score 800; DB 11; Length 4527;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 522 CGAGCTGAGGATTTGTCAGATCATCATCTCGTGTGAGTGAATGATGTTGGTGG 581  
DB 100 CGAGCTGAGGATTTGTCAGATCATCATCTCGTGTGAGTGAATGATGTTGGTGG 159  
QY 582 TGATCAGTGTCTGCTGAGGCACTACAGAGCTGTGACGCTCTTATCAGCGGAGCA 641  
DB 160 TGATCAGTGTCTGCTGAGGCACTACAGAGCTGTGACGCTCTTATCAGCGGAGCA 219  
QY 642 GCCAGGCGGAGGAGAGATGCTCTCTCTCAGAGATGCTGTGCGCTTGGCCCTCGGAGA 701  
DB 220 GCCAGGCGGAGGAGAGATGCTCTCTCTCAGAGATGCTGTGCGCTTGGCCCTCGGAGA 279  
QY 702 GCACAGTGTCTGAGGCAAGGAAATCCCAAGCGCGAGGCTTACGCGCCCTCGGAGCG 761  
DB 280 GCACAGTGTCTGAGGCAAGGAAATCCCAAGCGCGAGGCTTACGCGCCCTCGGAGCG 339  
QY 762 AGCGCTGAGCGGCGCGCCCTTGGCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCACT 821  
DB 340 AGCGCTGAGCGGCGCGCCCTTGGCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCACT 399  
QY 822 ATCCGTACTCTGAGACGAGATCCGACCTGCGACCCACATCTGCTGTCAGACGGGAGG 881  
DB 400 ATCCGTACTCTGAGACGAGATCCGACCTGCGACCCACATCTGCTGTCAGACGGGAGG 459  
QY 882 AGCCCCCACTTACCGAGGCGCCCTTCCAGCCCTTCCAGCTTCCAGGAGCGAGCTGG 941  
DB 460 AGCCCCCACTTACCGAGGCGCCCTTCCAGCCCTTCCAGCTTCCAGGAGCGAGCTGG 519  
QY 942 AACTGAAACCGGAGGTGCGTGGCGGACCCCGCAACCAACATCTTCCAGCTGACTGA 1001  
DB 520 AACTGAAACCGGAGGTGCGTGGCGGACCCCGCAACCAACATCTTCCAGCTGACTGA 579  
QY 1002 TGGATAGTCCAGGCTGCGGCGGCGCCCTGCGCGAGAGTAACTCGGGCATCGCGGCA 1061











CC method of inhibiting the growth of a prostate cancer cell; (3) a method  
 CC of modulating the expression of a gene in a prostate cancer cell; where  
 CC transcription of the gene is regulated by an androgen receptor; (4) a  
 CC method for diagnosing or prognosing prostate cancer; (5) a method of  
 CC screening for compounds that specifically bind to (1); and (6) a method  
 CC of evaluating the efficacy of a treatment in a patient with prostate  
 CC cancer. (1) has cytostatic activity, and can be used in gene therapy. (1)  
 CC polypeptides and polynucleotide can be used in reducing the expression of  
 CC an androgen receptor in a prostate cancer cell, inhibiting the growth of  
 CC a prostate cancer cell, modulating the expression of a gene in a prostate  
 CC cancer cell, diagnosing or prognosing prostate cancer, evaluating the  
 CC efficacy of a treatment in a patient with prostate cancer, treating  
 CC hyperproliferative and hypoproliferative disorders or in gene therapy.

XX. Sequence 759 BP, 152 A, 269 C, 226 G, 112 T, 0 U, 0 Other;

Query Match 57.2%; Score 755; DB 10; Length 759;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 581  
 DB CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 64  
 QY 582 TGATCAGTGTCTGTGACCACTACAGCTGTTCAGAGCTTTCATCAGCCGCA 641  
 DB 65 TGATCAGTGTCTGTGACCACTACAGCTGTTCAGAGCTTTCATCAGCCGCA 124  
 QY 642 GCCAGGGGCGAGAGAGAGAGATGCGCTTCTCAGAGAGATGCTGTGGCCCTCGAGA 701  
 DB 125 GCCAGGGGCGAGAGAGAGAGATGCGCTTCTCAGAGAGATGCTGTGGCCCTCGAGA 184  
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCGCCACCG 761  
 DB 185 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTACGCCCGCTCGCCACCG 244  
 QY 762 ACCGCTGCGCCGCTTTCGCCAGAGGGAGGCTTTCACCGCTTTCAGCCCACT 821  
 DB 245 ACCGCTGCGCCGCTTTCGCCAGAGGGAGGCTTTCACCGCTTTCAGCCCACT 304  
 QY 822 ATCCGACTGAGCAGAGATGCACTTCCACCACTCTGCTGTGACAGCGGAGG 881  
 DB 305 ATCCGACTGAGCAGAGATGCACTTCCACCACTCTGCTGTGAGAGGGAGG 364  
 QY 882 AGCCCCCACCCTTACAGAGCCCTTGCACCTTCAGGTTGCGAGACCCGAGCAGACTGG 941  
 DB 365 AGCCCCCACCCTTACAGAGCCCTTGCACCTTCAGGTTGCGAGACCCGAGCAGACTGG 424  
 QY 942 AACTGAACCGGAGTGTGTGCGGCAACCCCAAGAACATCTTTCAGACATGACTGA 1001  
 DB 425 AACTGAACCGGAGTGTGTGCGGCAACCCCAAGAACATCTTTCAGACATGACTGA 484  
 QY 1002 TGGATGTGTGCGGAGTGTGTGCGGAGCCCTGCCCCCGAGATGATCTGAGGAGTCA 1061  
 DB 485 TGGATGTGTGCGGAGTGTGTGCGGAGCCCTGCCCCCGAGATGATCTGAGGAGTCA 544  
 QY 1062 CGTGTCTACGCGAGCGGCGGAGTGAAGAGGGGCGCGCCCACTTACAGGAGTATCG 1121  
 DB 545 CGTGTCTACGCGAGCGGCGGAGTGAAGAGGGGCGCGCCCACTTACAGGAGTATCG 604  
 QY 1122 GCCACTACCGGGGCTCTCTTTCAGACACAGAGAGAGTGGGCGCCCTCTTCTGTGG 1181  
 DB 605 GCCACTACCGGGGCTCTCTTTCAGACACAGAGAGAGTGGGCGCCCTCTTCTGTGG 664  
 QY 1182 AGGGGAGCCGGGCTTCAACACACACATGCGCCCTTGAAGAGCGAGCATTTGAGCA 1241  
 DB 665 AGGGGAGCCGGGCTTCAACACACACATGCGCCCTTGAAGAGCGAGCATTTGAGCA 724  
 QY 1242 AAGAGAAGATTAACAGAAAGAGCAACCTCTCTAG 1276  
 DB 725 AAGAGAAGATTAACAGAAAGAGCAACCTCTCTAG 759

# RESULT 27

ID ADH62277 standard; cDNA; 759 BP.

AC ADH62277;

DT 25-MAR-2004 (first entry)

DE Human PMEPA1 coding cDNA.

KW Androgen-regulated gene; ARG, PMEPA1, therapy; diagnosis; prognosis;  
 KW prostate cancer; hormonal therapy; human; chromosome 20q13; gene; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 1..759  
 FT /\*tag= a  
 FT /product= "Human PMEPA1 protein"

PN US2003170713-A1.

PD 11-SEP-2003.

PF 18-MAR-2003; 2003US-00390045.

PR 28-JAN-2000; 2000US-0178772P.

PR 31-JAN-2000; 2000US-0179045P.

PR 26-JAN-2001; 2001US-00769482.

PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PI Srivastava S, Moul JW, Xu LL, Segawa T;

DR WPI; 2003-898255/82.

DR P-PSDB; ADH62211.

XX Polynucleotide array; useful for diagnosing or prognosing prostate  
 PT cancer; comprises a planar, non-porous solid support and a set of  
 PT polynucleotide probes attached to the solid support.

XX Claim 10; SEQ ID NO 2; 61pp; English.

CC The present invention relates to the identification and characterisation  
 CC of a novel androgen-regulated genes (ARGs) that exhibits abundant  
 CC expression in prostate tissue. The novel gene is designated PMEPA1. The  
 CC invention is useful for diagnosing and prognosing prostate cancer. The  
 CC invention is also useful in hormonal therapy. The present sequence is  
 CC human PMEPA1 coding cDNA. The PMEPA1 gene is located on chromosome 20q13.

XX. Sequence 759 BP, 152 A, 269 C, 226 G, 112 T, 0 U, 0 Other;

Query Match 57.2%; Score 755; DB 10; Length 759;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 581  
 DB 5 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 64  
 QY 582 TGATCAGTGTCTGTGACCACTACAGCTGTTCAGAGCTTTCATCAGCCGCA 641  
 DB 65 TGATCAGTGTCTGTGACCACTACAGCTGTTCAGAGCTTTCATCAGCCGCA 124  
 QY 642 GCCAGGGGCGAGAGAGAGATGCGCTTCTCAGAGAGATGCTGTGGCCCTCGAGA 701  
 DB 125 GCCAGGGGCGAGAGAGAGATGCGCTTCTCAGAGAGATGCTGTGGCCCTCGAGA 184  
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTACAGCCCGCTCGCCACCG 761  
 DB 185 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTACAGCCCGCTCGCCACCG 244  
 QY 762 ACCGCTGCGCCGCTTTCGCCAGAGGGAGGCTTTCACCGCTTTCAGCCCACT 821





RESULT 30  
ID AAA47429 standard; DNA; 1061 BP.  
AC AAA47429;  
XX 20-OCT-2000 (first entry)  
XX Sequence encoding human neuron-associated protein.  
XX  
XX Neuron associated protein; NEUAP; neurological disorder; epilepsy;  
KM ischemic cerebrovascular disease; stroke; cerebral neoplasm;  
KM Alzheimer's disease; Pick's disease; Huntington's disease; dementia;  
KM Parkinson's disease; demyelinating disease; meningitis; prion disease;  
KM kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;  
KM muscular dystrophy; central nervous system; CNS;  
KM peripheral nervous system; PNS; myopathy; schizophrenia;  
KM actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;  
KM cirrhosis; hepatitis; mixed connective tissue disease; MCTD;  
KM myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;  
KM autoimmune disease; inflammation; acquired immunodeficiency syndrome;  
KM AIDS; Addison's disease; adult respiratory distress syndrome; allergy;  
KM ankylosing spondylitis; amyloidosis; anaemia; asthma;  
KM Werner syndrome; trauma; human; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 101..859  
FT /tag=a  
FT /product="Neuron associated protein"  
XX  
XX MO200034477-A2.  
XX  
XX 15-JUN-2000.  
XX  
XX 10-DEC-1999; 99MO-US030408.  
XX  
XX 11-DEC-1998; 98US-00210083.  
XX 09-FEB-1999; 99US-0119365P.  
XX 16-MAR-1999; 99US-0124687P.  
XX  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-Young J;  
XX Yang J, Lu DM, Azimzai Y;  
XX WPI: 2000-423423/36.  
XX P-PSDB; AAB01388.  
XX  
XX New human neuron-associated proteins and polynucleotides encoding them,  
XX useful for diagnosis, treatment and prevention of cell proliferative  
XX disorders including cancer, neuronal and neurological disorders.  
XX  
XX Claim 9; Page 136; 145p; English.  
XX  
XX Human neuron-associated proteins (NEUAP) can be used for treating or  
XX preventing a disorder associated with decreased expression or activity of  
XX NEUAP. Antagonists of NEUAP are useful for treating or preventing  
XX disorder associated with increased expression or activity of NEUAP. NEUAP  
XX or their fragments or derivatives are useful for treating neurological  
XX disorder such as epilepsy, ischemic cerebrovascular disease, stroke,  
XX cerebral neoplasm, Alzheimer's disease, Pick's disease, Huntington's  
XX disease, dementia and Parkinson's disease. NEUAPs are also useful for  
XX treating other demyelinating diseases, bacterial and viral meningitis,  
XX prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and  
XX metabolic diseases of the nervous system, neurofibromatosis, other  
XX developmental disorders of the central nervous system, cerebral palsy,  
XX neuroskeletal disorders, autonomic nervous system disorders, cranial  
XX nerve disorders, spinal cord diseases, muscular dystrophy and other  
XX neuromuscular disorders, peripheral nervous system disorders, inherited,

CC metabolic, endocrine, and toxic myopathies, mental disorders including  
CC mood, anxiety and schizophrenic disorders, a cell proliferative disorder  
CC such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,  
CC cirrhosis, hepatitis, mixed connective tissue disease (MCTD),  
CC myelofibrosis, paroxysmal nocturnal haemoglobinuria, cancers of the  
CC adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, and an  
CC autoimmune/inflammatory disorder such as acquired immunodeficiency  
CC syndrome (AIDS). Addison's disease, adult respiratory distress syndrome,  
CC allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, Werner  
CC syndrome, complications of cancer, hemodialysis, and extracorporeal  
CC circulation, viral, bacterial, fungal parasitic, protozoal, and  
CC helminthic infections, and trauma. This sequence was given the Incyte ID  
CC no. 1871286CB1  
XX  
SQ Sequence 1061 BP; 225 A; 342 C; 326 G; 168 T; 0 U; 0 Other;  
Query Match 56.7%; Score 749; DB 3; Length 1061;  
Best Local Similarity 99.9%; Pired. No. 0;  
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 522 CGGAGCTGGAGTTGTTTCATATCATCATCGTGGTGGTGAATGGTATGGTGGTGG 581  
DB 105 CGAGCTGGAGTTGTTTCATATCATCATCGTGGTGGTGAATGGTATGGTGGTGG 164  
QY 582 TGATCAGTCCCTGCTGAGCCACTACAGCTGCTGACCGTCTTCATCAGCCGACCA 641  
DB 165 TGATCAGTCCCTGCTGAGCCACTACAGCTGCTGACCGTCTTCATCAGCCGACCA 224  
QY 642 GCCAGGGGGGAGAGAGAAAGATGCCCTGCTCAGAGAGATCCCTGGCCCTCGAGNA 701  
DB 225 GCCAGGGGGGAGAGAGAAAGATGCCCTGCTCAGAGAGATCCCTGGCCCTCGAGNA 284  
QY 702 GCACAGTGTGAGCAAGCAAGCAATCCAGAGCGGAGGTCTAGCCGCCCTCGGACCA 761  
DB 285 GCACAGTGTGAGCAAGCAAGCAATCCAGAGCGGAGGTCTAGCCGCCCTCGGACCA 344  
QY 762 ACCGCTGGCCGCTGCGCCCTTCGCCAGGGAGCGCTTCAACCGCTTCAAGCCCACT 821  
DB 345 ACCGCTGGCCGCTGCGCCCTTCGCCAGGGAGCGCTTCAACCGCTTCAAGCCCACT 404  
QY 822 ATCCGTAACCTGACAGCAGAGATGACCTGCAACCCACATCTGCTGACAGCGGGAGG 881  
DB 405 ATCCGTAACCTGACAGCAGAGATGACCTGCAACCCACATCTGCTGACAGCGGGAGG 464  
QY 882 AGCCCCCACTTACAGAGGCCCCCTGCAACCTTCAAGCTTGGGAGCCCCGACAGAGCTGG 941  
DB 465 AGCCCCCACTTACAGAGGCCCCCTGCAACCTTCAAGCTTGGGAGCCCCGACAGAGCTGG 524  
QY 942 AACTGAACCGGAGTGGTGGCGGCAACCCCAACAGAACCATCTTGAAGTGAAGTGA 1001  
DB 525 AACTGAACCGGAGTGGTGGCGGCAACCCCAACAGAACCATCTTGAAGTGAAGTGA 584  
QY 1002 TGGATAGTGCAGAGTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCCCA 1061  
DB 585 TGGATAGTGCAGAGTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGGCATCAGCCCA 644  
QY 1062 CGTGTACGCAAGCGGGGGGCGATGGAGGGGGCGGCGCCCACTACAGGAGGTCAATG 1121  
DB 645 CGTGTACGCAAGCGGGGGGCGATGGAGGGGGCGGCGCCCACTACAGGAGGTCAATG 704  
QY 1122 GCCACTACCGGGGGTCTCTTCCAGACAGCAGAGAGTGGGCGCCCTCTTGTGTGG 1181  
DB 705 GCCACTACCGGGGGTCTCTTCCAGACAGCAGAGAGTGGGCGCCCTCTTGTGTGG 764  
QY 1182 AGGGAGCCGGCTTCACACACACATCGGCCCTTGAAGGCGCAGCATCTGAGCA 1241  
DB 765 AGGGAGCCGGCTTCACACACACATCGGCCCTTGAAGGCGCAGCATCTGAGCA 824  
QY 1242 AAGGAAGATTAACAGAAAGACACCTCTTGAAGTCCCGAGGGGGCGGGCTGGGG 1301  
DB 825 AAGGAAGATTAACAGAAAGACACCTCTTGAAGTCCCGAGGGGGCGGGCTGGGG 884  
QY 1302 CTGCGTAGTGAAGAAAGCAG 1321















QY 642 GCCAGGGGGCGAGGAGAGAGATGCCCTGCTCTGAGAGAGATGCTGTGGCCCTCGAGGA 701  
DB 130 GCCAGGGGGCGAGGAGAGATGCCCTGCTCTGAGAGAGATGCTGTGGCCCTCGAGGA 189  
QY 702 GCACAGTGTCAAGGACAGGAATCCAGAGCCGAGGCTTACGCCCGCTTGGCCCAACG 761  
DB 190 GCACAGTGTCAAGGACAGGAATCCAGAGCCGAGGCTTACGCCCGCTTGGCCCAACG 249  
QY 762 ACCGCTGGCCGCTGCGCCCTTCCGCGAGGAGCGCTTCCAGCCGCTTCCAGCCCT 821  
DB 250 ACCGCTGGCCGCTGCGCCCTTCCGCGAGGAGCGCTTCCAGCCGCTTCCAGCCCT 309  
QY 822 ATCCGTACCTGACAGAGATGACCTGCGACCCACCATCTGCTGTCCAGACGAGGAGG 881  
DB 310 ATCCGTACCTGACAGAGATGACCTGCGACCCACCATCTGCTGTCCAGACGAGGAGG 369  
QY 882 AGCCCCCACTTACAGAGGCGCCCTGACACCTTCAAGCTTGGGAGCCCGAGCAGAGCTGG 941  
DB 370 AGCCCCCACTTACAGAGGCGCCCTGACACCTTCAAGCTTGGGAGCCCGAGCAGAGCTGG 429  
QY 942 AACTGAACCGGAGAGTGGTGGCGGACCCGCCAACAAGACATCTTGCAGAGTGA 1001  
DB 430 AACTGAACCGGAGAGTGGTGGCGGACCCGCCAACAAGACATCTTGCAGAGTGA 489  
QY 1002 TGGATAGTCCAGAGCTGGGCGGCGCCCTGCGACGATTAATCTGGGCGATCAGCGCCA 1061  
DB 490 TGGATAGTCCAGAGCTGGGCGGCGCCCTGCGACGATTAATCTGGGCGATCAGCGCCA 549  
QY 1062 CGTCTCAAGGACGCGCGGCGCATGTAGAGGCGCGCCGCCACCTACAGCAGAGTCAATCG 1121  
DB 550 CGTCTCAAGGACGCGCGGCGCATGTAGAGGCGCGCCGCCACCTACAGCAGAGTCAATCG 609  
QY 1122 GCCACTACCCGGGCTCTCTCTTCCAGACACAGCAGAGAGATGGGCGCCCTTCTTGGTGG 1181  
DB 610 GCCACTACCCGGGCTCTCTCTTCCAGACACAGCAGAGAGATGGGCGCCCTTCTTGGTGG 669  
QY 1182 AGGGGAGCCGGCTCCACACACACATCGGCGCCCTTGAAGAGCGGACCATCTGAGACA 1241  
DB 670 AGGGGAGCCGGCTCCACACACACATCGGCGCCCTTGAAGAGCGGACCATCTGAGACA 729  
QY 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCGGCTGGGG 1301  
DB 730 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCGGCTGGGG 789  
QY 1302 CTGCGTAGTGAAAAAGCAG 1321  
DB 790 CTGCGTAGTGAAAAAGCAG 809

RESULT 37  
ABS61424  
ID ABS61424 standard; cDNA, 1583 BP.  
XX AC ABS61424;  
XX DT 05-NOV-2002 (first entry)  
XX DE Prostate specific nucleic acid DEX0259\_32.  
XX KW Human; ss; prostate specific nucleic acid; PSNA; prostate cancer;  
XX KW cytostatic; non-cancerous prostate disease; PSP; vaccine;  
XX KW prostate specific protein; metastasis.  
OS Homo sapiens.  
XX OS  
XX PN WO200242776-A2.  
XX PD 30-MAY-2002.  
XX PF 01-NOV-2001; 2001WO-US045654.  
XX PR 01-NOV-2000; 2000US-0244782P.

PA (DIAD-) DIADEXUS INC.  
XX Sun Y, Reclipon H, Chen S, Liu C;  
PI WPI; 2002-490217/52.  
XX  
XX New polypeptide useful for diagnosing and monitoring the presence and  
PT metastases of prostate cancer in a patient and as a component in  
PT databases for search analysis as well as in sequence analysis algorithms.  
PS Claim 1; Page 166-167; 242pp; English.  
XX  
XX The invention relates to an isolated polypeptide comprising a sequence  
CC with 60 % identity to one of prostate specific protein (PSP) sequences,  
CC or comprising an amino acid sequence encoded by one of 136 nucleotide  
CC prostate specific nucleic acid sequences, PSNA, (or a sequence that  
CC hybridises to it or is 60% identical to it), given in the specification.  
CC Also included are a vector comprising the polynucleotide, a host cell  
CC comprising the vector, an antibody specific for the PSP proteins and a  
CC vaccine comprising the protein or polynucleotide. The PSP and PSNA are  
CC useful for diagnosing and monitoring the presence and metastases of  
CC prostate cancer in a patient. The PSNA is useful for determining the  
CC level PSNA in a sample. An antibody to the PSP is useful for determining  
CC the presence of prostate specific protein in a sample, and for treating a  
CC patient with prostate cancer, which induces an immune response against  
CC the prostate cancer cell expressing the nucleic acid or polypeptide and a  
CC kit is useful for detecting a risk of cancer or presence of cancer in a  
CC patient. PSNA is useful as hybridisation probes to detect, characterise  
CC and quantify hybridising nucleic acids from both genomic and transcript-  
CC derived nucleic acid samples and also in microarrays. Sequences of PSP  
CC and PSNA are useful as components in databases for search analysis as  
CC well as in sequence analysis algorithms. PSNA is useful to drive in vivo  
CC expression of PSP. The present sequence is a PSNA of the invention  
XX  
SQ Sequence 1583 BP; 361 A; 469 C; 457 G; 296 T; 0 U; 0 Other;  
Query Match 42.4%; Score 560; DB 6; Length 1583;  
Best Local Similarity 100.0%; Pred. No. 3.7e-240;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 730 GCGGAGGTCTAAGCGCCCGCTTGGCCGACCGCTGAGCGCGCTTGGCCCA 789  
DB 827 GCGGAGGTCTAAGCGCCCGCTTGGCCGACCGCTGAGCGCGCTTGGCCCA 886  
QY 790 GCGGAGCGCTTCCAGCGCTTCCAGCGCCCACTTACCTTCCAGAGAGATCCACCT 849  
DB 887 GCGGAGCGCTTCCAGCGCTTCCAGCGCCCACTTACCTTCCAGAGAGATCCACCT 946  
QY 850 GCCACCCACCATCTGCTGTCAAGCGGGAGAGAGCCGCCACCTTACAGAGGCGCTGAC 909  
DB 947 GCCACCCACCATCTGCTGTCAAGCGGGAGAGAGCCGCCACCTTACAGAGGCGCTGAC 1006  
QY 910 CTTCCAGCTTGGGAGCCCGAGCAGCAGCTGAATCTGAACCGGAGTGGTGGCGGACCC 969  
DB 1007 CTTCCAGCTTGGGAGCCCGAGCAGCAGCTGAATCTGAACCGGAGTGGTGGCGGACCC 1066  
QY 970 CCCAAACAGAACATCTTCCAGCAGTGAACCTGATGAGATGAGCCAGGCTGGGCGCCCTG 1029  
DB 1067 CCCAAACAGAACATCTTCCAGCAGTGAACCTGATGAGATGAGCCAGGCTGGGCGCCCTG 1126  
QY 1030 CCCCCCAGAGTAATCTGGGAGCATCAGCGCACGCTGTACAGGAGCGGCGGCGCATGA 1089  
DB 1127 CCCCCCAGAGTAATCTGGGAGCATCAGCGCACGCTGTACAGGAGCGGCGGCGCATGA 1186  
QY 1090 GGGGCGCGCCGACCTTACAGCGAGTCAATCGGCACTACCCGGAGTCTTCCAGCA 1149  
DB 1187 GGGGCGCGCCGACCTTACAGCGAGTCAATCGGCACTACCCGGAGTCTTCCAGCA 1246  
QY 1150 CCAGCAGAGAGTGGGCGCGCTTCTTGTCTGAGAGGAGACCCGGTCCACACACACAT 1209  
DB 1247 CCAGCAGAGAGTGGGCGCGCTTCTTGTCTGAGAGGAGACCCGGTCCACACACACAT 1306  
QY 1210 CCGGCGCCTTAGAGAGCGGAGCATCTGAGAGAAAGAGATTAACAGAAAGACACCC 1269



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QY 413 ATGACCGCTTATGATGGGGGTCAAGACGACCGCGCGCGCGGGGACCGCAATGTC 472
DB 411 ATGACCGCTTATGATGGGGGTCAAGACGACCGCGCGCGCGGGGACCGCAATGTC 352
QY 473 TCCTGCACTGCACTGCACTGCAAAAGCTCTTTGTTCCAGAGCATGAGATCA 521
DB 351 TCCTGCACTGCACTGCACTGCAAAAGCTCTTTGTTCCAGAGCATGAGATCA 303

RESULT 39
ADN98767/c
ID ADN98767 standard; cDNA; 711 BP.
XX
AC ADN98767;
XX
DT 29-JUL-2004 (first entry)
XX
DE Novel human cDNA sequence #367.
XX
KM ds; gene; anti-inflammatory; dermatologically, neuroprotective;
KM immunomodulator; antibacterial; virucide; antipsoriatic; cytostatic;
KM gene therapy; vaccine; inflammatory; CNS; immune disorder; cancer;
KM psoriasis; diabetes; early aging; hormonal imbalance;
KM ischemic heart disease; ulcerative colitis.
XX
OS Homo sapiens.
XX
PN W02004038003-A2.
XX
PD 06-MAY-2004.
XX
PE 24-OCT-2003; 2003WO-US033947.
XX
PR 25-OCT-2002; 2002US-0421061P.
PR 25-OCT-2002; 2002US-0421080P.
PR 25-OCT-2002; 2002US-0421552P.
PR 25-OCT-2002; 2002US-0421614P.
PR 30-OCT-2002; 2002US-0422177P.
PR 30-OCT-2002; 2002US-0422178P.
PR 15-NOV-2002; 2002US-0426355P.
PR 15-NOV-2002; 2002US-0426384P.
PR 15-NOV-2002; 2002US-0426394P.
PR 15-NOV-2002; 2002US-0426430P.
PR 15-NOV-2002; 2002US-0426916P.
PR 27-NOV-2002; 2002US-0428222P.
PR 27-NOV-2002; 2002US-0428275P.
PR 27-NOV-2002; 2002US-0429302P.
PR 27-NOV-2002; 2002US-0429326P.
PR 27-NOV-2002; 2002US-0429651P.
PR 04-DEC-2002; 2002US-0430645P.
PR 04-DEC-2002; 2002US-0430651P.
PR 04-DEC-2002; 2002US-0430657P.
PR 04-DEC-2002; 2002US-0430663P.
PR 04-DEC-2002; 2002US-0430668P.
PR 05-DEC-2002; 2002US-0430684P.
PR 05-DEC-2002; 2002US-0430937P.
PR 05-DEC-2002; 2002US-0430965P.
PR 05-DEC-2002; 2002US-0431458P.
PR 12-DEC-2002; 2002US-0433251P.
PR 12-DEC-2002; 2002US-0433500P.
PR 13-DEC-2002; 2002US-0433316P.
PR 13-DEC-2002; 2002US-0433318P.
PR 23-DEC-2002; 2002US-0436236P.
PR 03-JAN-2003; 2003US-0437914P.
PR 17-JAN-2003; 2003US-0440820P.
PR 17-JAN-2003; 2003US-0440821P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
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PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476621P.
PR 09-JUN-2003; 2003US-0476632P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485217P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485359P.
PR 08-JUL-2003; 2003US-0485359P.
PR 14-JUL-2003; 2003US-0486466P.
PR 14-JUL-2003; 2003US-0486460P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
XX Halenbeck RF, Kochakota S, Lin H, Limmemann T, Pierce K, Wang Y;
XX Pi Wong JGP, Wu G, Zhang H, Zeng C;
XX
DR WPI; 2004-365511/34.
XX
DR P-PSDB; ADN98551.
XX
PS New nucleic acid molecules, useful in preparing a composition for
XX treating or preventing e.g. inflammatory, CNS, bacterial or viral
XX disorders, cancer, psoriasis, diabetes, ischemic heart disease or
XX ulcerative colitis.
XX
PS Claim 1; SEQ ID NO 367; 532bp; English.
XX
XX The invention relates to a nucleic acid molecule comprising a
XX polynucleotide sequence or its complement that encodes a polypeptide. The
XX nucleic acid is useful in preparing a composition for treating or
XX preventing inflammatory, CNS, immune, bacterial or viral disorder,
XX cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
XX heart disease or ulcerative colitis. This sequence corresponds to a
XX nucleic acid of the invention.
SQ
Sequence 711 BP; 97 A; 230 C; 279 G; 105 T; 0 U; 0 Other;

Query Match 31.0%; Score 409; DB 12; Length 711;
Best Local Similarity 100.0%; Pred. No. 1.3e-172; Indels 0; Gaps 0;
Matches 409; Conservative 0; Mismatches 0;

QY 113 TCAGCCCCGGGCGAGGCGCGCGCCCGCTGCAAGCCATTTCGAGCGCACCCGGGG 172
DB 711 TCAGCCCCGGGCGAGGCGCGCGCCCGCTGCAAGCCATTTCGAGCGCACCCGGGG 652
QY 173 CACTGCCAGCGCCCGCGGCGCTGCGAGGAGGCGCGGCGCGCGAGCGCGGCTC 232
DB 651 CACTGCCAGCGCCCGCGGCGCTGCGAGGAGGCGCGGCGCGCGAGCGCGGCTC 592
QY 233 CCGGCACTGAGCCCGCGGCGCGCGCGCGGGAATTGGGGGAGCCCGCGAGCCG 292
DB 591 CCGGCACTGAGCCCGCGGCGCGCGCGCGGGAATTGGGGGAGCCCGCGAGCCG 532
QY 293 GGGGCGGCTCCCGCGCGCGCGCGCTCTGATCGGAGGCGCCAGCTCCGGGCGCGGCG 352
DB 531 GGGGCGGCTCCCGCGCGCGCGCGCTCTGATCGGAGGCGCCAGCTCCGGGCGCGGCG 472
QY 353 GGAAGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGC 412
DB 471 GGAAGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGC 412
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QY 413 ATGCACCCCTGATGAGGGGCTCAACGACACCGCCGCCGCCGCCGAGCCCAATGTC 472  
DB 411 ATGCACCCCTGATGAGGGGCTCAACGACACCGCCGCCGCCGCCGAGCCCAATGTC 352  
QY 473 TCCGTCAGCTGCACTGCAACGCTCTTGTTCAGAGCATGAGATGA 521  
DB 351 TCTGCACTGCACTGCAACGCTCTTGTTCAGAGCATGAGATGA 303

## RESULT 40

AAF65983  
ID AAF65983 standard: cDNA, 408 BP.

AAF65983;  
AC AAF65983;  
DT 09-APR-2001 (first entry)

DE Novel human polynucleotide, SEQ ID NO: 1739.

KM Human; cytoslastic; gene therapy; colon cancer; prostate cancer;  
KM breast cancer; lung cancer; cancer detection; ss.

XX Homo sapiens.

XX WO200102568-A2.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000MO-US018374.

XX 02-JUL-1999; 99US-0142310P.

XX 02-JUL-1999; 99US-0142311P.

XX (CHIR ) CHIRON CORP.

XX (HYSE-) HYSEQ INC.

PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;  
PI Kassam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G,  
PI Drmanac R, Klenjakov R, Drmanac S, Dickson M, Labat I;  
PI Leshkowitz D, Kila D, Garcia V, Jones LW, Strache-Crain B;

XX WPI; 2001-091805/10.

PT Library of polynucleotides for diagnosing a cancerous state of a  
PT mammalian cell and detecting cancer, particularly of the colon or  
PT prostate, comprises 3351 human polynucleotide sequences.

PS Claim 9; Page 793; 1046pp; English.

XX The present sequence is one of 3351 sequences in a library of human  
XX polynucleotides. The library is used to detect differentially expressed  
XX genes correlated with a cancerous state of a mammalian cell and can  
XX detect colon, prostate, breast and lung cancer. The library can be used  
XX to produce probes for detection of mRNA and to produce additional copies  
XX of the polynucleotides. The probes can be used for chromosome mapping of  
XX the polynucleotide and for detection of transcription levels. Ribozymes  
XX or antisense oligonucleotides can be generated. The polynucleotides and  
XX their gene products are used as genetic or biochemical markers (e.g. in  
XX blood or tissues) that will detect the earliest changes along the  
XX carcinogenesis pathway and/or monitor the efficacy of therapies and  
XX preventive interventions. The polynucleotides, polypeptides and  
XX antibodies against them can be used in pharmaceutical compositions to  
XX treat the cancers and proliferative disorders such as neoplasia,  
XX dysplasia and hyperplasia

XX Sequence 408 BP; 81 A; 159 C; 115 G; 53 T; 0 U; 0 Other;

XX Query Match 30.4%; Score 401; DB 5; Length 408;

XX Best Local Similarity 100.0%; Pred. No. 5.3e-169;

XX Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 GATCAGCTGCTGCTGAGCCACTACAAAGCTGTCTGACAGGCTCTTATCAGCCGACAG 642

DB 8 GATCAGCTGCTGCTGAGCCACTACAAAGCTGTCTGACAGGCTCTTATCAGCCGACAG 67  
QY 643 CCAGGGGCGAGAGAGAAATGCTCTCTCAAGAAATGCTGTGGCCCTGGAGAG 702  
DB 68 CCAGGGGCGAGAGAGAAATGCTCTCTCAAGAAATGCTGTGGCCCTGGAGAG 127  
QY 703 CACAGTGTCAAGGCAACGAAATCCAGAGCCGAGAGCTTACGCCCTGGCCACCGA 762  
DB 128 CACAGTGTCAAGGCAACGAAATCCAGAGCCGAGAGCTTACGCCCTGGCCACCGA 187  
QY 763 CCGCTGAGCGCTGCGCCCTTCCGAGCGGAGCGCTTCCAGCCCTCACTTA 822  
DB 188 CCGCTGAGCGCTGCGCCCTTCCGAGCGGAGCGCTTCCAGCCCTCACTTA 247  
QY 823 TCCGTACTGCAAGACAGATTCAGCTCCAGCCCAATCTGCTGACAGCGGGAGGA 882  
DB 248 TCCGTACTGCAAGACAGATTCAGCTCCAGCCCAATCTGCTGACAGCGGGAGGA 307  
QY 883 GCCCCACCTTACAGAGGAGCCCTGCACTTCCAGCTTCCAGAGCAGAGCTTGA 942  
DB 308 GCCCCACCTTACAGAGGAGCCCTGCACTTCCAGCTTCCAGAGCAGAGCTTGA 367  
QY 943 ACTGAACCGGAGTCTGCTGCGGACCCCAACAGAACCA 983  
DB 368 ACTGAACCGGAGTCTGCTGCGGACCCCAACAGAACCA 408

## RESULT 41

ACL59789  
ID ACL59789 standard: cDNA, 408 BP.

XX ACL59789;  
AC ACL59789;

XX 24-MAR-2005 (first entry)

DE Human colon cancer differentially expressed polynucleotide, SEQ ID:5924.

KM Differential expression; diagnosis; therapy; drug screening; cancer;  
KM neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;  
KM ss.

XX Homo sapiens.

XX WO200500087-A2.

XX 06-JAN-2005.

XX 13-MAY-2004; 2004MO-US015421.

XX 03-JUN-2003; 2003US-0475872P.

XX (CHIR ) CHIRON CORP.

PI Randazzo F, Moler E, Escobedo J, Garcia PD;

XX WPI; 2005-075421/08.

PT New isolated polynucleotides, which are differentially expressed in colon  
PT cancer cell, useful for treating cancer, e.g. colon cancer, breast  
PT cancer, or pancreatic cancer.

PS Claim 1; SEQ ID NO 5924; 97pp; English.

XX The invention relates to 9672 polynucleotides (ACL53866-ACL63537) which  
XX are differentially expressed in colon cancer cells. The invention also  
XX relates to vectors and host cells comprising a differentially expressed  
XX polynucleotide of the invention; a method for detecting a cancerous cell  
XX by detection of a gene product of the polynucleotides; a method for  
XX inhibiting a cancerous phenotype of a cell by inhibiting a gene product  
XX of the polynucleotides; a method of treating an individual with cancer by  
XX administration of a modulator of a gene product of the polynucleotides;  
XX and an isolated antibody that specifically binds to a polypeptide encoded





PF 21-AUG-2001; 2001WO-US026089.  
XX  
XX 22-AUG-2000; 2000US-0227159P.  
XX  
XX (BGM ) BRIGHAM & WOMENS HOSPITAL INC.  
XX (PIZ ) PFIZER INC.  
XX  
XX Lee RT, Landeschulz KT, Kennedy SP, Thompson JF, Turi TG;  
XX WPI; 2002-280912/32.  
XX  
XX Novel nucleic acid molecule encoding Mechanically Induced Vascular  
XX Receptor-1 polypeptide, useful for treating cardiovascular diseases.  
XX  
XX Disclosure; Page 101; 105pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule encoding a  
XX Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having  
XX cardiac cell anti-apoptotic activity and fragments of it provided they  
XX are not identical to Genbank sequences A1761441.1, A1594390, NM\_004338  
XX and A0777461. Also included are expression vectors, host cells, the MIVR-  
XX 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting  
XX a molecule having cardiac cell anti-apoptotic activity with a candidate  
XX agent, where the molecule is a nucleic acid molecule comprising MIVR-1,  
XX IEX-1, VDRP-1, BNG-2 and TIS-11d or its expression product, determining  
XX if the anti-apoptotic activity is modulated and thereby identifying a  
XX modulator. The cardiac cell anti-apoptotic molecules and nucleic acids  
XX of the invention are useful for treating, diagnosing and monitoring  
XX progression of such diseases and disorders as characterised by increased  
XX apoptotic cell-death of vascular endothelial cells e.g. cardiac  
XX hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart  
XX failure. The present sequence is one of the four human MIVR-1 and which  
XX are specifically disclaimed  
XX  
XX Sequence 693 BP; 101 A; 205 C; 237 G; 149 T; 0 U; 1 Other;  
SQ

Query Match 22.9%; Score 302; DB 6; Length 693;  
Best Local Similarity 100.0%; Pred. No. 9.8e-125;

Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 885 CCCCACTTACAGGAGGCCCCCTGACCTTCAGAGCTTGGGAGACCCGAGAGAGAGTGAAC 944  
DB 587 CCCCACTTACAGGAGGCCCCCTGACCTTCAGAGCTTGGGAGACCCGAGAGAGAGTGAAC 528  
QY 945 TGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGTCTGATGG 1004  
DB 527 TGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGTCTGATGG 468  
QY 1005 ATAGTGCAGAGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGTCTGATGG 1064  
DB 467 ATAGTGCAGAGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGTCTGATGG 408  
QY 1065 GCTACGGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1124  
DB 407 GCTACGGAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348  
QY 1125 ACTACCGGAGTCTCTTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1184  
DB 347 ACTACCGGAGTCTCTTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 288  
QY 1185 GG 1186  
DB 287 GG 286

RESULT 45

AAZ52964  
ID AAZ52964 standard; cDNA; 812 BP.

XX AAZ52964;  
AC  
XX

DT 14-MAR-2000 (first entry)

XX  
DE Human prostate tumor cDNA library derived EST fragment #107.  
XX  
XX Pancreas; tumor; EST; expressed sequence tag; human; cytosolic;  
XX treatment; ds.  
XX  
XX Homo sapiens.  
XX  
XX DE19820190-A1.  
XX  
XX 04-NOV-1999.  
XX  
XX 28-APR-1998; 98DE-01020190.  
XX  
XX 28-APR-1998; 98DE-01020190.  
XX  
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.  
XX  
XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;  
XX WPI; 1999-621386/54.  
XX P-PSDB; AAY74135, AAY74136, AAY74137.  
XX  
XX New human nucleic acid sequences from pancreatic tumors, and related  
XX proteins.  
XX  
XX Claim 2; Page 269-270; 502pp; German.  
XX  
XX This invention describes novel polypeptides and their encoding nucleic  
XX acids derived from human pancreatic tumor tissue which have cytostatic  
XX activity. The sequences are also useful in producing pharmaceutical  
XX compositions for treatment of pancreatic tumors. AAZ52858-253014  
XX represent expressed sequence tag (EST) fragments derived from a human  
XX pancreatic tumor cDNA library and which encode the proteins represented  
XX in AAY73814-Y74252  
XX  
XX Sequence 812 BP; 157 A; 272 C; 237 G; 146 T; 0 U; 0 Other;  
SQ

Query Match 20.5%; Score 271; DB 2; Length 812;  
Best Local Similarity 99.7%; Pred. No. 7.2e-111;

Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 644  
DB 426 TCAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 485  
QY 645 AGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 704  
DB 486 AGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 545  
QY 705 CAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 764  
DB 546 CAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 605  
QY 765 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 824  
DB 606 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 665  
QY 825 CGTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 884  
DB 666 CGTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 725  
QY 885 CCCCACTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 906  
DB 726 CCCCACTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747

RESULT 46

AAA41265  
ID AAA41265 standard; cDNA; 254 BP.

XX AAA41265;  
AC  
XX





XX Homo sapiens.  
OS  
XX US2003073623-A1.  
XX  
XX 17-APR-2003.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX 30-JUL-2001; 2001US-00918995.  
XX  
XX (DRMANAC R T.  
PA (LABAT I.  
PA (STACHE-CRAIN B.  
PA (DICKSON M C.  
PA (JONES L W.  
XX  
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
PI  
XX  
XX WPI; 2003-615964/58.  
XX  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.  
XX  
XX  
XX Claim 1; SEQ ID NO 2074; 44bp; English.  
XX  
XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC segdata.uspto.gov/sequence.html?DocID=20030073623  
XX  
XX  
SQ Sequence 467 BP; 133 A; 121 C; 131 G; 74 T; 0 U; 8 Other;  
Query Match 13.5%; Score 178; DB 9; Length 467;  
Best Local Similarity 100.0%; Pred. No. 3e-69;  
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 36 CCAGCACCCGACGAGAGTGGCCCGCCCTCTGCTGAGGGGACCCGGCTCCACCACAC 95  
QY 1204 ACACATCGCGCCCTGAGAGGCGCAGCATCTGAGCAAGAAAGATTAACAGAAAG 1263  
DB 96 ACACATCGCGCCCTGAGAGGCGCAGCATCTGAGCAAGAAAGATTAACAGAAAG 155  
QY 1264 ACACCTCTCTAGAGTCCCGAGGGGGCGGGCTGGGGCTGCGTAGGTAAAAAGGCGAG 1321  
DB 156 ACACCTCTCTAGAGTCCCGAGGGGGCGGGCTGGGGCTGCGTAGGTAAAAAGGCGAG 213

Search completed: February 28, 2006, 10:42:32  
Job time : 826 secs



**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:02:46 ; Search time 5833 Seconds  
(without alignments)  
10595.874 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcgagctcgcgagcga.....ctgcgtagctgaagcag 1321

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 2339354128 residues

Word size: 23

Total number of hits satisfying chosen parameters: 16459

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hic:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gsa1:  
10: gb\_gsa2:  
11: gb\_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	741	56.1	901	4	CR612083 full-length
2	632	47.8	1046	3	BM922276 AGENCOURT
3	614	46.5	967	5	BQ641849 AGENCOURT
4	588	44.5	647	8	DN992322 TC124411
5	568	43.0	916	5	BQ954555 AGENCOURT
6	558	42.2	609	5	BQ636742 hdl3h06.y
7	550	41.6	551	3	BM141979 if2sa11.y
8	542	41.0	601	8	DN991959 TC113206
9	536	40.6	605	7	CV028567 7115 Full
10	533	40.3	850	1	AL558881 AL558881
11	518	39.2	729	5	BQ575741 UI-H-EZ1-
12	511	38.7	850	5	BQ602918 AGENCOURT
13	497	37.6	890	5	BQ690750 AGENCOURT
14	474	37.5	553	8	DN990606 TC121025
15	474	35.9	572	5	BX641317 DXF2686K
16	471	35.7	1068	5	BUS27705 AGENCOURT
17	468	35.4	655	5	BQ681705 AGENCOURT
18	450	34.1	964	5	BQ859860 AGENCOURT
19	449	34.0	945	5	BUS39219 AGENCOURT
20	445	33.7	782	3	BQ015170 UI-H-ED1-
21	442	33.5	602	6	CA431191 UI-H-FG1-
22	442	33.5	780	10	AY119334 Homo sapi

23	441	33.4	461	3	BM712680 UI-E-E30-
24	437	33.1	633	3	BM714472 UI-E-E30-
25	428	32.4	588	3	BQ624784 UI-H-RC1-
26	425	32.2	897	1	AL558882 AL558882
27	424	32.1	1038	1	AL517150 AL517150
28	422	31.9	844	5	BQ686793 AGENCOURT
29	422	31.9	938	5	BUI57842 AGENCOURT
30	422	31.9	952	5	BUI57959 AGENCOURT
31	422	31.9	1280	5	BQ691500 AGENCOURT
32	417	31.6	659	5	BE855409 UI-E-C11-
33	417	31.6	529	5	BUI730650 UI-E-C11-
34	406	30.7	1400	3	BM559329 AGENCOURT
35	401	30.4	730	3	BM677602 UI-CF-E01
36	399	30.2	626	7	BM974296 UI-CF-E01
37	395	29.9	544	7	CN296134 UI-CF-E01
38	393	29.8	728	5	BQ683523 UI-CF-E01
39	390	29.5	973	5	BUI69156 AGENCOURT
40	383	29.0	570	5	BQ575582 UI-H-EZ1-
41	377	28.5	563	6	CB049800 NISC.g113
42	365	27.6	552	3	BM713900 UI-E-E30-
43	358	27.1	1127	5	BUI74654 AGENCOURT
44	348	26.3	646	5	BQ859841 AGENCOURT
45	338	25.6	867	5	BX362396 BX362396
46	331	25.1	899	5	BUI96912 AGENCOURT
47	327	24.8	547	3	BM676516 UI-E-E30-
48	324	24.5	613	2	BG680325 602629217
49	302	22.9	651	6	CB554226 MMSPP0052-
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51	291	22.0	502	1	AI921394 w024c07.x
52	288	21.8	668	6	CB044866 NISC.gC07
53	286	21.7	446	3	BM681946 UI-E-E01-
54	283	21.4	437	1	AI936228 w03e04.x
55	280	21.2	990	6	CB108549 K-EST0148
56	277	21.0	277	6	CD367193 UI-H-FT2-
57	268	20.3	618	6	BM705514 UI-E-C11-
58	257	19.5	308	3	AI493698 qy97c07.x
59	246	18.6	451	1	AI885001 w188c11.x
60	243	18.4	518	1	AA917446 0151d08.x
61	239	18.1	453	1	AI377498 lc37c07.x
62	239	18.1	588	1	AI744327 w950f07.x
63	239	17.8	619	1	BE138909 xw97f09.x
64	235	17.8	380	2	CA418897 UI-H-EZ1-
65	232	17.6	705	6	AM452945 UI-H-BT1-
66	230	17.4	397	2	BF46904 UI-H-BT1-
67	225	17.0	463	5	BUI739449 UI-E-E30-
68	225	17.0	430	1	AM204238 UI-H-BT1-
69	225	17.0	463	2	BF939262 nad86D06.
70	225	17.0	674	1	AI972096 w162d11.x
71	225	17.0	381	1	AM135998 UI-H-BT1-
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73	222	16.8	1264	5	BQ877825 AGENCOURT
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76	218	16.5	457	1	AI1369306 qy91e08.x
77	218	16.5	464	2	AI928027 w127b11.x
78	217	16.4	404	1	AI928027 w127b11.x
79	216	16.4	889	5	BQ883225 AGENCOURT
80	216	16.4	524	1	AI640802 c171g09.x
81	215	16.3	242	3	BM767985 K-EST0050
82	209	15.8	221	3	BM768155 K-EST0051
83	208	15.7	624	2	BG897912 HOA26-1-B
84	198	15.0	990	2	BG675643 603622053
85	198	15.0	342	1	AI521341 c105b09.x
86	197	14.9	392	6	CB144148 K-EST0198
87	196	14.8	338	6	AI826012 w42g04.x
88	194	14.7	634	1	AA595115 n032b02.x
89	188	14.2	508	1	AA007283 w154e08.x
90	179	13.6	467	1	AA088701 z183f05.x
91	177	13.4	438	1	BG323347 602421734
92	175	13.2	857	2	BUI73052 UI-E-C11-
93	174	13.2	454	1	AA027926 zK05h07.x
94	171	12.9	386	2	BF475759 n0c41b07.x
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Qy	707	GTGTACGGCAACGAAATCCCAAGAGCCGAGGCTTACGGCCGCTCGGACCAAGACCGC	766
Db	361	GTGTACGGCAACGAAATCCCAAGAGCCGAGGCTTACGGCCGCTCGGACCAAGACCGC	420
Qy	767	CTGACCGGTGCGGACCTTTGCGCCAGCGGAGGCGCTTCAACCGCTTCAAGCCCACTTATCG	826
Db	421	CTGACCGGTGCGGACCTTTGCGCCAGCGGAGGCGCTTCAACCGCTTCAAGCCCACTTATCG	480
Qy	827	TACCTGCAAGCAAGAAATGAACTGTGCAACCCAACTCTGACGTGTCAAGAGGGAGAGGACCC	886
Db	481	TACCTGCAAGCAAGAAATGAACTGTGCAACCCAACTCTGACGTGTCAAGAGGGAGAGGACCC	540
Qy	887	CCACCCCTTACCAAGGAGCCCTGTGCAACCTTCAGATTCTGGGAAACCCGAGCAACAGCTGGAACTG	946
Db	541	CCACCCCTTACCAAGGAGCCCTGTGCAACCTTCAGATTCTGGGAAACCCGAGCAACAGCTGGAACTG	600
Qy	947	AACCGGGAAGTCGGTGCGGCGCAACCCCAACAGAACCAATCTTTGACAGTGACCTGATGGAT	1006
Db	601	AACCGGGAAGTCGGTGCGGCGCAACCCCAACAGAACCAATCTTTGACAGTGACCTGATGGAT	660
Qy	1007	AGTGCACAGCTTGGAGGCGCCCTGTGCCCCCAGCAATTAATCTGGGGGATCAAGCGCCACGTGCG	1066
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Db	721	TACGCGACGGGCGG 734	

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LOCUS	B0641849
DEFINITION	B0641849 967 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265 5', mRNA sequence.
ACCESSION	B0641849
VERSION	B0641849.1 GI:21766021
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
REFERENCE	1 (bases 1 to 967) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strusberg, Ph.D. Email: cgabbs@mail.nih.gov
TITLE	Tissue Procurement: ATCC
JOURNAL	cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
COMMENT	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.novartis.com">http://image.lnl.novartis.com</a> Plate: LNCX2493 row: g column: 18 High quality sequence stop: 571. location/Qualifiers 1..967
FEATURES	
source	Source

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FEATURES
SOURCE
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_id="NH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald W. Rudin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

```

```

ORIGIN
      (Stratagene) and Superscript II RT (Life Technologies) .
      Note: this is a NIH_MGC Library.  | "
Query Match      46.5%;   Score 614;   DB 5;   Length 967;
Query Local Similarity  99.7%;
      Pred. No. 3,2e-201;
Matches 714;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

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[illegible]

RESULT 4	
DN992322	
LOCUS	647 bp mRNA linear EST 17-MAY-2005
DEFINITION	TC124411 Human adult whole brain, large insert, PCMV expression library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEDAI), transcript variant 4, mRNA sequence.
ACCESSION	DN992322
VERSION	DN992322.1 GI:66252153
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo
REFERENCE	1 (bases 1 to 647)







DB 541 CTCTTCTGAGGAGGACCCGCTCCACCAACAATCGGCCCCCTTAGAGGCGCAGC 600  
 QY 1231 CATCTGAG 1239  
 DB 601 CATCTGAG 609

RESULT 7  
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 LOCUS BM141979  
 DEFINITION cDNA clone IMAGE:5677341 5' similar to TR:Q9UDJ3 Q9UDJ3 D071807.1  
 ; mRNA sequence.  
 BM141979  
 ACCESSION BM141979.1 GI:17152046  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 551)  
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Biscorn, A.,  
 Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,  
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., R.,  
 Williams, T., Jackson, Y., and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Juliana Brown  
 (brownjefas.harvard.edu) This sequence now available from the IMAGE  
 consortium, for clone orders contact: info@image.llnl.gov  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 429.  
 Location/Qualifiers  
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 /dev\_stage="Adult"  
 /lab\_host="DH10B"  
 /clone\_lib="Melton Normalized Human Islet 4 N4-HIS 1"  
 /note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;  
 Site 2: Sal 1; Starting library constructed using  
 SuperScript Plasmid Library kit (Life Technologies). cDNA  
 made by oligo-dT priming. Size-selected by column  
 fractionation; average insert size 1.08 kb. Library was  
 amplified once on solid support and plasmid DNA from  
 library was prepared. The library DNA was normalized by  
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
 Research 6:791-806; 0.5 microgram single-stranded library  
 plasmid DNA was mixed with 5 micrograms PCR product  
 representing library inserts and hybridized to an Ecot of  
 20. Single-stranded (unhybridized) plasmids were isolated  
 by hydroxyapatite chromatography and used to make this  
 library."

Query Match 41.6%; Score 550; DB 3; Length 551;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-259;  
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QY 714 GCAACGAAATCCAGAGCCGACAGTCTACGCCCCGCTCGGCCACCGACCGCTGAGCG 773  
 DB 1 GCAACGAAATCCAGAGCCGACAGTCTACGCCCCGCTCGGCCACCGACCGCTGAGCG 60  
 QY 774 TGCCGCTTTCGCGCCAGCGGAGCGCTTCCAGCGCTTTCAGGCCCACTATTCGTAACCTGC 833  
 DB 61 TGCCGCTTTCGCGCCAGCGGAGCGCTTCCAGCGCTTTCAGGCCCACTATTCGTAACCTGC 120  
 QY 834 AGCAGGATGACCTGCGCACCCACCATCTGCTGTCAGCGGGAGAGAGCCCACTT 893  
 DB 121 AGCAGGATGACCTGCGCACCCACCATCTGCTGTCAGCGGGAGAGAGCCCACTT 180  
 QY 894 ACCAGGCCCCCTGACACCTTCACGCTTCGAGACCCGACGACGAGCTGAACTGAACCGAG 953  
 DB 181 ACCAGGCCCCCTGACACCTTCACGCTTCGAGACCCGACGAGCTGAACTGAACCGAG 240  
 QY 954 AGTCGCTGCGGACACCCCAAGAAACATCTTTCAGCACTGACCTGATGATGATGCCA 1013  
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 QY 1014 GGCTGGGCGGCGCCCTGCGCCCGCCAGAGTAATCGGGATCAGCGCCAGCTGACGCA 1073  
 DB 301 GGCTGGGCGGCGCCCTGCGCCCGCCAGAGTAATCGGGATCAGCGCCAGCTGACGCA 360  
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 QY 1134 GGTCTCTCTTCCAGACACGACGAGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGG 1193  
 DB 421 GGTCTCTCTTCCAGACACGACGAGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 QY 1194 TCCACGACACACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1253  
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 DB 541 AACGAAAGG 550

RESULT 8  
 DN991959 601 bp mRNA linear EST 17-MAY-2005  
 LOCUS DN991959  
 DEFINITION TC113206 Human adult whole brain, large insert, PCMV expression  
 library Homo sapiens cDNA clone TC113206 5' similar to Homo sapiens  
 transmembrane, prostate androgen induced RNA (TMPRI), transcript  
 variant 1, mRNA sequence.  
 DN991959  
 ACCESSION DN991959.1 GI:66251790  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 601)  
 Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,  
 Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,  
 Zhang, X., Jay, G., and He, W.  
 High-throughput cloning of full-length human cDNAs directly from  
 cDNA libraries optimized for large and rare transcripts  
 Unpublished (2005)  
 CONTACT: Kovacs, K.  
 High Throughput cDNA Cloning  
 Origene Technologies, Inc. (www.origene.com)  
 6 Taft Court, Suite 100, Rockville, MD 20850, USA  
 Tel: 301 340 3188  
 Fax: 301 340 8606

TITLE  
 JOURNAL  
 COMMENT



OY	757	CACCGACCGCGCTGGCGCGCGCCCTTGCGCCAGGAGGAGGCGCTTCCACCGGCTTCAGAGC	816
Db	195	CACCGACCGCGCTGGCGCGCGCCCTTGCGCCAGGAGGAGGCGCTTCCACCGGCTTCAGAGC	254
OY	817	CACCTATCCGTACCTTGACGACAGAGATGCACTTGCACCCACCATCTGCGTGTGACAGCG	876
Db	255	CACCTATCCGTACCTTGACGACAGAGATGCACTTGCACCCACCATCTGCGTGTGACAGCG	314
OY	877	GAGGAGGCCCCCAACCTTACAGAGGCGCCCTTGACACCTTCCAGCTTCGGGAGCCCGAGACAGCA	936
Db	315	GAGGAGGCCCCCAACCTTACAGAGGCGCCCTTGACACCTTCCAGCTTCGGGAGCCCGAGACAGCA	374
OY	937	GCTGGACCTGAAACCGGAGATGCGGTGCGGCAACCCCAACAGAAACATCTTGAAGTGA	996
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OY	997	CCTGATGATATGTGTCAGGAGCTGGGCGGCCCTTGACCCCCACAGCACTAACCTGGGATCAG	1056
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OY	1117	CATGGGACCACTAACCGGGGCTCTCTTCCAGACACAGACAGAGCAATG	1163
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AL558881/c	AL558881	850 bp	mRNA	linear	EST 02-APR-2004
LOCUS	AL558881				
DEFINITION	Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED				
	Homo sapiens cDNA clone CSD0015712 3-PRIME, mRNA sequence.				

ACCESSION	AL558881	GI:46184268
VERSION	AL558881.3	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Genoscope  
Genoscope - Centre National de Séquençage  
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: [segregt@genoscope.cns.fr](mailto:segregt@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pOWSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9945.r  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna7b=CS0DDU015DC06NP1&c=9945.r>

FEATURES	Location/Qualifiers
source	1. .850

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODJ015YP12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_id="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Bclor V

```

ORIGIN	sites of the pOWNSPORT 6 vector. Library was normalized."
Query Match	40.3%; Score 533; DB 1; Length 850;
Best Local Similarity	99.5%; Pred. No. 3e-51;
Matches 733; Conservative	0; Mismatches 4; Indels 0; Gaps 0

QY	585	TCACGTGCTCTGCTAGGACCACTTACAGACTGTCTGCAAGCTCTCTTATCAAGCCGGACACACC	644
Db	846	TCACGTGCTCTGCTAGGACCACTTACAGACTGTCTGCAAGCTCTCTTATCAAGCCGGACACACC	787
QY	645	AGGGGCGGAGAGAGAATAGTCCCTGTCTCTCAGAAAGATGTGCTGTGGCCCTCGAGAGACA	704
Db	786	AGGGGCGGAGAGAGAATAGTCCCTGTCTCTCAGAAAGATGTGCTGTGGCCCTCGAGAGACA	727
QY	705	CAGTGTCAAGGCMAACGAAATCCCAAGAGCCGACAGTCTACGCCCCGCTTCGACCCACGACCC	764
Db	726	CAGTGTCAAGGCMAACGAAATCCCAAGAGCCGACAGTCTACGCCCCGCTTCGACCCACGACCC	667
QY	765	GCCGTGCGCTGTGCGCCCTTTCGCCCCAGCGGAGCGCTTCCACCGCTTCCAGGCCACCTATTC	824
Db	666	GCCGTGCGCTGTGCGCCCTTTCGCCCCAGCGGAGCGCTTCCACCGCTTCCAGGCCACCTATTC	607
QY	825	CGTACCTTGACACACGAGATTCGACCTGACCCACCATCTGCTGTACAGCGGAGAGAGAC	884
Db	606	CGTACCTTGACACACGAGATTCGACCTGACCCACCATCTGCTGTGTACAGCGGAGAGAGAC	547
QY	885	CCCCACCCCTTACAGAGGCCCTCTGCAACCTTCAGCTTCGGAGACCCCGAGCAGCAGCTGGAAAC	944
Db	546	CCCCACCCCTTACAGAGGCCCTCTGCAACCTTCAGCTTCGGAGACCCCGAGCAGCAGCTGGAAAC	487
QY	945	TGAAACCGGGAATCGGTGTGCGGCCACCCCTCAACAGAACCATTTGTGACAGTGAACCTTGATGG	1000
Db	486	TGAAACCGGGAATCGGTGTGCGGCCACCCCTCAACAGAACCATTTGTGACAGTGAACCTTGATGG	427
QY	1005	ATTAGTGCAGAGCTGTGGGCGGCGCCCTTGACCCGCCAGCAGATTAATTGCGGCAATCAAGCCGCACT	1060
Db	426	ATTAGTGCAGAGCTGTGGGCGGCGCCCTTGACCCGCCAGCAGATTAATTGCGGCAATCAAGCCGCACT	367
QY	1065	GCTACCGGCAAGCGGCGGCGGCGCATGTGAGAGGCGCGCGGCCACCTTACAGCGAGGTCAATCGGCC	1122
Db	366	GCTACCGGCAAGCGGCGGCGGCGCATGTGAGAGGCGCGCGGCCACCTTACAGCGAGGTCAATCGGCC	307
QY	1125	ACTTACCGGGGGTTCCTCTTCCAGACACAGCAGAGAGATGTGGGCGCGCCCTTCTGTGAGAGG	1188
Db	306	ACTTACCGGGGGTTCCTCTTCCAGACACAGCAGAGAGATGTGGGCGCGCCCTTCTGTGAGAGG	247
QY	1185	GGACCCGGCTCCACCAACACACATTCGCGCCCTTGAAGAGCGCAGCCATTGTGAGCAAG	1244
Db	246	GGACCCGGCTCCACCAACACACATTCGCGCCCTTGAAGAGCGCAGCCATTGTGAGCAAG	187
QY	1245	AGAAAGATTAACAGAAAGAGACACCTCTCTTAGGGTCCCAAGGGGGGCGGGCTGTGGGCTTG	1300
Db	186	AGAAAGATTAACAGAAAGAGACACCTCTCTTAGGGTCCCAAGGGGGGCGGGCTGTGGGCTTG	127
QY	1305	CGTAGGTGAAGAAAGCAG	1321
Db	126	CGTAGGTGAAGAAAGCAG	110

RESULT 11					
LOCUS	B0575741/c				
DEFINITION	B0575741	729 bp	mRNA	linear	EST 19-JUN-2007
ACCESSION	UI-H-E21-bbg-h-14-0-UI.s1	NCI CGAP Ch2	Homo sapiens	cDNA clone	
VERSION	UI-H-E21-bbg-h-14-0-UI 3'			mRNA sequence.	
KEYWORDS	B0575741				
SOURCE	B0575741.1	GI:21479058			
ORGANISM	EST.				
	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				















[illegible][illegible]



LOCUS	AV419334	780 bp	DNA linear	GSS 17-DEC-2003
DEFINITION	Homo sapiens TM6P1 gene, VIRUAL TRANSCRIPT, partial sequence.			
ACCESSION	AV419334			
VERSION	AV419334.1 GI:3975291			
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 780) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Ciavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.			
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE	2 (bases 1 to 780)			
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Ciavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.			
FEATURES	Location/Qualifiers			
SOURCE	1..780			
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" "1..>780" /gene="TM6P1" /locus_tag="HCM6856"			
ORIGIN	Query Match 33.5%; Score 442; DB 10; Length 780; Best Local Similarity 100.0%; Pred. No. 2.3e+206; Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	835 GCACGAGATCGACCTGCGACCCACCATCTCGCTGTGACGCGGGAGAGGCCCCACCTTA 894			
DB	339 GCACGAGATCGACCTGCGACCCACCATCTCGCTGTGACGCGGGAGAGGCCCCACCTTA 398			
QY	895 CCAGGGCCCTTGACCTTCCAGCTTGGGAGCCCGAGCGAGCGTGGAACTGAACCCGGGA 954			
DB	399 CCAGGGCCCTTGACCTTCCAGCTTGGGAGCCCGAGCGAGCGTGGAACTGAACCCGGGA 458			
QY	955 GTGCGGCGCGGACCCCAAGAACATCTTCCAGCTGACCTGATGATGATGTCGAG 1014			
DB	459 GTGCGGCGCGGACCCCAAGAACATCTTCCAGCTGACCTGATGATGATGTCGAG 518			
QY	1015 GCTGGGCGGCGCCCTGCGCCCGGACGAGTAATCTGGGCATCAGCGCCACGTGCTACGGCAG 1077			
DB	519 GCTGGGCGGCGCCCTGCGCCCGGACGAGTAATCTGGGCATCAGCGCCACGTGCTACGGCAG 578			
QY	1075 CGGCGGGCGCATGGAGGGGGCGCGCCCACTACAGCGAGGTCATCTGGGCACTAACCCGGG 1133			
DB	579 CGGCGGGCGCATGGAGGGGGCGCGCCCACTACAGCGAGGTCATCTGGGCACTAACCCGGG 638			
QY	1135 GTCTCTCTTCAGACACAGACAGACAGTGGGCGCGCTCTTGTGCTGGAGGGGACCCGGCT 1199			
DB	639 GTCTCTCTTCAGACACAGACAGACAGTGGGCGCGCTCTTGTGCTGGAGGGGACCCGGCT 698			
QY	1195 CCACGACACACATCGCGCGCCCTTAGAGAGCGGACCATCTGAGACAAAGAGAGATTA 1255			
DB	699 CCACGACACACATCGCGCGCCCTTAGAGAGCGGACCATCTGAGACAAAGAGAGATTA 758			
QY	1255 ACAGAAAGACACCTCTCTTAG 1276			

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Db          759  ACAGAAAGACACCTCTCTAG  780
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RESULT 23
BM712680
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PUBMED
FEATURES
SOURCE

```

461 bp mRNA linear EST 28-FEB-2002  
 BM712680  
 UI-E-EJO-abg-a-10-0-UI.r1 UI-E-EJO Homo sapiens CDNA clone  
 UI-E-EJO-abg-a-10-0-UI 5', mRNA sequence.  
 BM712680  
 BM712680.1 GI:19025938  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 461)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 8889548  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: Bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.iesgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. 461  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-EJO-abg-a-10-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Foveal and Macular, RPE and  
 Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-EJO"  
 /note="Organ: eye; Vector: pTT73-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-E-EJO is a subcloned CDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand CDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded CDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pTT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand CDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes,  
 AGATTCAGCA; lens, CGATTCAGCA; eye anterior segment,  
 AATGCCGAT; optic nerve, CATTTCAGTG; retina, CCGCG; Retina  
 Foveal and Macular, GTCC, RPE and Choroid, ACCCTA. This  
 library was created for the program, Gene Discovery in the  
 Visual System, supported by National Eye Institute (NEI).

33.4%; Score 441; DB 3; Length 461;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-206; Indels 0; Gaps 0  
 Matches 441; Conservative 0; Mismatches 0;

881 GAGCCCCACCACTACGAGGCCCTCCAGCTTCGCGGACCCCGAGCAGCAGCTG 940

```

Db      1 GAGCCCCCACTTACAGAGGCCCCCTGCACTTCAGCTTCGGAGACCCCGAGACAGACTG 60
Qy      941 GAACGTAAACCGGAGTGGTGGTGGCGGACACCCCAACAGAACCATCTTGACAGTACCTG 1000
Db      61 GAACGTAAACCGGAGTGGTGGTGGCGGACACCCCAACAGAACCATCTTGACAGTACCTG 120
Qy      1001 ATGATTAAGTGCAGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1060
Db      121 ATGATTAAGTGCAGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Qy      1061 ACGTCTACAGGCGAGGCGGCGGCGATGAGAGGGGCGCGCGCCACCTACAGAGAGTATC 1120
Db      181 ACGTCTACAGGCGAGGCGGCGGCGATGAGAGGGGCGCGCGCCACCTACAGAGAGTATC 240
Qy      1121 GGGCACTACCGCGGGGCTCTCTCTTCCAGCAGCAGCAGCAGTGGCGCGCTCTTGGCTG 1180
Db      241 GGGCACTACCGCGGGGCTCTCTCTTCCAGCAGCAGCAGCAGTGGCGCGCTCTTGGCTG 300
Qy      1181 GAGGGGAGCCGGGCTTCCACACACACATCGCGCCCTTACAGAGGCGAGCCATCTGGAGC 1240
Db      301 GAGGGGAGCCGGGCTTCCACACACACATCGCGCCCTTACAGAGGCGAGCCATCTGGAGC 360
Qy      1241 AAAGAGAGATTAACAGAAAGAGACACCTCTCTAGAGGTCCCGAGGGGGGGCGGCTGGG 1300
Db      361 AAAGAGAGATTAACAGAAAGAGACACCTCTCTAGAGGTCCCGAGGGGGGGCGGCTGGG 420
Qy      1301 GCTGCTAGTGTGAAAGGCGAG 1321
Db      421 GCTGCTAGTGTGAAAGGCGAG 441

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RESULT 24
LOCUS      BM714472                633 bp      mRNA      linear      EST 28-FEB-2002
DEFINITION UI-E-EU0-shs-f-20-0-UI_r1 UI-E-EU0 Homo sapiens cDNA clone
VERSION     BM714472.1 GI:19027730
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE   1 (bases 1 to 633)
AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
           discovery
JOURNAL     Genome Res. 6 (9), 791-806 (1996)
PUBMED     8889548
COMMENT     Contact: Soares, MB
           Coordinated Laboratory for Computational Genomics
           University of Iowa
           375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
           Tel: 319 335 8250
           Fax: 319 335 9565
           Email: bento-soares@uiowa.edu
           Tissue Procurement: Dr. Gregg Hageman
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Researchers may obtain clones from Research
           Genetics (www.reagen.com).
           The following repetitive elements were found in this cDNA
           sequence: 593-614, >AT rich#Low_complexity (matched complement)
           Seq primer: M13 Reverse

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FEATURES
SOURCE      1. 633
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
           /clone="UI-E-EU0-shs-f-20-0-UI"

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/tissue type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev stage="fetal and adult"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-E-EU0"
/note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EU0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pRTT3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGATCAGAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGCAT; optic nerve, CCATTAACTG; retina, CCGCG; Retina
Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
```

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ORIGIN
Query Match      33.1%; Score 437; DB 3; Length 633;
Best Local Similarity 100.0%; Pred. No. 6,8e-204;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      885 CCCCACTTACAGAGGCCCCCTGACACCTTCAGCTTGGGAGCCCCGAGACAGCTGGAGC 944
Db      14 CCCCACTTACAGAGGCCCCCTGACACCTTCAGCTTGGGAGCCCCGAGACAGCTGGAGC 73
Qy      945 TGAACCGGAGTGGTGGTGGCGGACACCCCAACAGAACCATCTTGACAGTACCTGATGG 1004
Db      74 TGAACCGGAGTGGTGGTGGCGGACACCCCAACAGAACCATCTTGACAGTACCTGATGG 133
Qy      1005 ATATGTCAGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1064
Db      134 ATATGTCAGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 193
Qy      1065 GCTACGCGACAGGCGGCGGCGATGAGAGGGGCGCGCCACCTACAGCGAGTATCGGCC 1124
Db      194 GCTACGCGACAGGCGGCGGCGATGAGAGGGGCGCGCCACCTACAGCGAGTATCGGCC 253
Qy      1125 ACTACCGGGGCTCTCTTCCAGCAGCAGAGCACTGAGCGGCTCTTGGTGGAGG 1184
Db      254 ACTACCGGGGCTCTCTTCCAGCAGCAGAGCACTGAGCGGCTCTTGGTGGAGG 313
Qy      1185 GAGCCGGGCTCCACACACACATCGCGGCCCTTAGAGAGCGAGCATGTGAGCAAG 1244
Db      314 GAGCCGGGCTCCACACACACATCGCGGCCCTTAGAGAGCGAGCATGTGAGCAAG 373
Qy      1245 AGAAGATTAACAGAAAGACACCTCTTAGAGGTCCCGAGGGGGCGGGCTGGGGCTG 1304
Db      374 AGAAGATTAACAGAAAGACACCTCTTAGAGGTCCCGAGGGGGCGGGCTGGGGCTG 433
Qy      1305 CGTAGGTGAAAGGCGAG 1321
Db      434 CGTAGGTGAAAGGCGAG 450

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RESULT 25
LOCUS      BU624784/c                588 bp      mRNA      linear      EST 23-SEP-2002
DEFINITION UI-H-FG1-bgl-f-22-0-UI_s1 NCI CGAP FG1 Homo sapiens cDNA clone
VERSION     BU624784.1 GI:23290999
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```







TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LCM2387 row: e column: 05  
High quality sequence stop: 593.  
Location/Qualifiers

## FEATURES

source

1. 844  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6248044"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 31.9%; Score 422; DB 5; Length 844;  
Best Local Similarity 100.0%; Pred. No. 1.7e-196;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

900 GCCCTGCACTCCCTCCAGCTTGGGACCCCGACAGCAGTGAACCTGAACCGGGAGTGG 959  
1 GCCCTGCACTCCCTCCAGCTTGGGACCCCGACAGCAGTGAACCTGAACCGGGAGTGG 60

960 TGGCGGCACTCCCAAGCAACATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1019  
61 TGGCGGCACTCCCAAGCAACATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120

1020 GCGGCCCCCTGCCCCCGACAGTAACTCGGCGATCAGCGCACTGCTACGCGAGCGGG 1079  
121 GCGGCCCCCTGCCCCCGACAGTAACTCGGCGATCAGCGCACTGCTACGCGAGCGGG 180

1080 GCGGCGATGAGGGGCGCGCGCCCACTTACAGCGAGTCACTGGCCACTTACCGGGGTCT 1139  
181 GCGGCGATGAGGGGCGCGCGCCCACTTACAGCGAGTCACTGGCCACTTACCGGGGTCT 240

1140 CTTTCAGACACGAGCAGAGCAGTGGGCGCCCTCTTGTGAGAGGGGACCCGGCTCAAC 1199  
241 CTTTCAGACACGAGCAGAGCAGTGGGCGCCCTCTTGTGAGAGGGGACCCGGCTCAAC 300

1200 ACACACATCGCGCCCTTGAAGAGCGACCATCTGAGCAAGAAGAAAGATTAACAGA 1259  
301 ACACACATCGCGCCCTTGAAGAGCGACCATCTGAGCAAGAAGAAAGATTAACAGA 360

1260 AAGGACACCTCTTGAAGGTCCCGAGGGGGCGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1319  
361 AAGGACACCTCTTGAAGGTCCCGAGGGGGCGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 420

1320 AG 1321  
421 AG 422

RESULT 29  
BU157842 938 bp mRNA linear EST 04-SRP-2002  
LOCUS BU157842  
DEFINITION AGENCOURT\_7976988 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6081573

5', mRNA sequence.  
ACCESSION BU157842  
VERSION BU157842.1 GI:22671752  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 938)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC

## FEATURES

source

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LCM2308 row: 1 column: 22  
High quality sequence stop: 423.  
Location/Qualifiers

## ORIGIN

source

1. 938  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6081573"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_110"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

Query Match 31.9%; Score 422; DB 5; Length 938;  
Best Local Similarity 100.0%; Pred. No. 1.7e-196;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

900 GCCCTGCACTCCCTCCAGCTTGGGACCCCGACAGCAGTGAACCTGAACCGGGAGTGG 959  
1 GCCCTGCACTCCCTCCAGCTTGGGACCCCGACAGCAGTGAACCTGAACCGGGAGTGG 60

960 TGGCGGCACTCCCAAGCAACATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1019  
61 TGGCGGCACTCCCAAGCAACATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120

1020 GCGGCCCCCTGCCCCCGACAGTAACTCGGCGATCAGCGCACTGCTACGCGAGCGGG 1079  
121 GCGGCCCCCTGCCCCCGACAGTAACTCGGCGATCAGCGCACTGCTACGCGAGCGGG 180

1080 GCGGCGATGAGGGGCGCGCGCCCACTTACAGCGAGTCACTGGCCACTTACCGGGGTCT 1139  
181 GCGGCGATGAGGGGCGCGCGCCCACTTACAGCGAGTCACTGGCCACTTACCGGGGTCT 240

1140 CTTTCAGACACGAGCAGAGTGGGCGCCCTCTTGTGAGAGGGGACCCGGCTCAAC 1199  
241 CTTTCAGACACGAGCAGAGTGGGCGCCCTCTTGTGAGAGGGGACCCGGCTCAAC 300

1200 ACACACATCGCGCCCTTGAAGAGCGACCATCTGAGCAAGAAGAAAGATTAACAGA 1259  
301 ACACACATCGCGCCCTTGAAGAGCGACCATCTGAGCAAGAAGAAAGATTAACAGA 360

1260 AAGGACACCTCTTGAAGGTCCCGAGGGGGCGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1319

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Db      361 AAGGACACCTCTGTAGGGGTCCCAAGGGGGCGGGCTGGGGCTGCGTAGTGAAGAGGC 420
Qy      1320 AG 1321
Db      421 AG 422

RESULT 30
BUI57959
LOCUS   BUI57959          952 bp      mRNA      linear      EST 04-SEP-2002
DEFINITION AGENCOURT_8076058 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084984
5', mRNA sequence.
ACCESSION BUI57959
VERSION   BUI57959.1 GI:22671869
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo
          1 (bases 1 to 952)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          JOURNAL Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: rgs@bbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHCW2317 row: k column: 01
          High quality sequence stop: 607.
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            1..952
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              /db_xref="taxon:9606"
              /clone="IMAGE:6084984"
              /tissue_type="ductal carcinoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_110"
              /note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
              Site:2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

ORIGIN
Query Match      31.9%; Score 422; DB 5; Length 952;
Best Local Similarity 100.0%; Pred. No. 1.7e-196; Indels 0; Gaps 0;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      900 GCCCTGACACCTCTGAGTTCGGGACCCCGAGACAGACCTGGAACCTGAACCGGGAGTGG 959
Db      1 GCCCTGACACCTCTGAGTTCGGGACCCCGAGACAGACCTGGAACCTGAACCGGGAGTGG 60

Qy      960 TGGCGGACACCCCAAGAACATCTTGACAGTGCATGATGATGATGTCGCGAGGCTGG 1019
Db      61 TGGCGGACACCCCAAGAACATCTTGACAGTGCATGATGATGATGTCGCGAGGCTGG 120

Qy      1020 GGGGGCCCTGGCCCCCGAGACAGTAACTGGGGCATAGGCCACGCTTAAGGCGAGCGGCG 1079
Db      121 GGGGGCCCTGGCCCCCGAGACAGTAACTGGGGCATAGGCCACGCTTAAGGCGAGCGGCG 180

Qy      1080 GGGCGATGAGAGGGGGCGCGCCACCTACAGCGAGTGCATCGGCCACTTAACCGGGGCTCT 1139
Db      181 GGGCGATGAGAGGGGGCGCGCCACCTACAGCGAGTGCATCGGCCACTTAACCGGGGCTCT 240

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```

Qy      1140 CTTTCAGACACGACAGAGAGGAGGGCCGCTCTTGTGCTGAGGGAGACCCGGCTCCACC 1199
Db      241 CTTTCAGACACGACAGAGAGGAGGGCCGCTCTTGTGCTGAGGGAGACCCGGCTCCACC 300

Qy      1200 ACACACATCGCGCCCTTAGAGAGCGACGACCTCTGAGACAAAGAAAGATTAACAGA 1259
Db      301 ACACACATCGCGCCCTTAGAGAGCGACGACCTCTGAGACAAAGAAAGATTAACAGA 360

Qy      1260 AAGGACACCTCTCTTAGGGTCCCGAGGGGGCGGGGCTGGGGCTGCGTAGTGAAGAGGC 1319
Db      361 AAGGACACCTCTCTTAGGGTCCCGAGGGGGCGGGGCTGGGGCTGCGTAGTGAAGAGGC 420

Qy      1320 AG 1321
Db      421 AG 422

RESULT 31
B0691500
LOCUS   B0691500          1280 bp      mRNA      linear      EST 15-JUL-2002
DEFINITION AGENCOURT_9345477 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248217
5', mRNA sequence.
ACCESSION B0691500
VERSION   B0691500.1 GI:21816816
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homiidae; Homo
          1 (bases 1 to 1280)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          JOURNAL Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: rgs@bbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LHCW2387 row: 1 column: 10
          High quality sequence stop: 423.
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              /clone_lib="NIH_MGC_110"
              /note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
              Site:2: EcoRI; cDNA made by oligo-dT priming.
              Directionally cloned into EcoRI/XhoI sites using the
              following 5' adaptor: GGCACGAG(G). Library constructed by
              Ling Hong in the laboratory of Gerald M. Rubin (University
              of California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

ORIGIN
Query Match      31.9%; Score 422; DB 5; Length 1280;
Best Local Similarity 100.0%; Pred. No. 1.6e-196; Indels 0; Gaps 0;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      854 CCACCATCTTCGCTGTAGAGAGGGGAGAGAGCCCGACCTTAACAGAGGCGCCCTGCACTTC 913
Db      28 CCACCATCTTCGCTGTAGAGAGGGGAGAGAGCCCGACCTTAACAGAGGCGCCCTGCACTTC 87

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QY	914	AGGTTGGGAGCCCGAGCAGAGTGGAACTGAAACGGAGAGTGGGTGCGGCACCCCA	973
Db	88	CAGCTTGGGAGCCCGAGCAGAGTGGAACTGAAACGGAGAGTGGGTGCGGCACCCCA	147
QY	974	AACAGAACCATCTTTCGACAGTGAACCTGATGATATGTGCAGAGCTGGGCGGCCCTTCGCC	1033
Db	148	AACAGAACCATCTTTCGACAGTGAACCTGATGATATGTGCAGAGCTGGGCGGCCCTTCGCC	207
QY	1034	CCGAGCACTAACCTGGGGCATCAGCGGCCACGTGCTAACCGGCACGCGGGCGCATGGAGGGG	1093
Db	208	CCGAGCACTAACCTGGGGCATCAGCGGCCACGTGCTAACCGGCACGCGGGCGCATGGAGGGG	267
QY	1094	CGCGCGCCCACTACAGGAGAGTCATCGGCCACTACCGGGGGTCTCTCTTCAGACACAG	1153
Db	268	CGCGCGCCCACTACAGGAGAGTCATCGGCCACTACCGGGGGTCTCTCTTCAGACACAG	327
QY	1154	CAGAGCAGTGGGCGCGCCCTCTCTGTGTGAGGGGAGCCGGCTTCCACACACACATCGCG	1213
Db	328	CAGAGCAGTGGGCGCGCCCTCTCTGTGTGAGGGGAGCCGGCTTCCACACACACATCGCG	387
QY	1214	CCCTTAGAGAGCGCAGCCATCTGTGAGCAAAAGAGAGTAAACAGAAAGGACACCCCTCTC	1273
Db	388	CCCTTAGAGAGCGCAGCCATCTGTGAGCAAAAGAGAGTAAACAGAAAGGACACCCCTCTC	447
QY	1274	TA 1275	
Db	448	TA 449	

LOCUS DEFINITION	BE855409	559 bp	mRNA	linear	EST 29-SEP-2000
BE855409/c	BE855409				
LOCUS	7913f05.x1	NCI_CGAP	Brim3	Homo sapiens	CDNA clone IMAGE:3306369 3'
DEFINITION	similar to TR:Q9JUD3	Q9JUD3	DU718d7.1	;	mRNA sequence.

ACCESSION	BB855409
VERSION	BB855409.1
KEYWORDS	GI:10367404
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Home sapiens

REFERENCE	1 (bases 1 to 559)
AUTHORS	NCI/NIHDS-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/STGAP), Tumor Gene Index
JOURNAL	Unpublished (1998)
COMMENT	Contact: Robert Strausberg, Ph.D.

JOURNAL  
 COMMENT  
 Unpublished (1998)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from G1bco  
 High quality sequence stop: 443.  
 Location/Qualifiers  
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FEATURES
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TGTTATCCATTCTAAGGGAGGCGGCACATCTTTTTTTTTTTTTTTTTT  
T3'}; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI' sites of the modified pRTS vector.  
Library is normalized, and was constructed by Bento  
Soares and M.Fatima Bonaldo."

[illegible]

**RESULT 33**  
**BUT730650/c**  
**LOCUS**  
**DEFINITION** BU-B-CII-afg-o-09-0-ui.s1 ui-B-CII Homo sapiens cDNA clone  
**ACCESSION** BU730650  
**VERSION** BU730650.1 GI:23654753  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 629)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
**JOURNAL**  
**PUBLISHED** 8889548  
**COMMENT** Contact: Soares, MB

Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@iowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)).

Seq primer: M13 FORWARD  
POLYA=Yes  
FEATURES  
Source

Location/Qualifiers  
1..629  
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/mol\_type="mRNA"  
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/clone="UI-E-C11-afg-o-09-0-UI"  
/tissue\_type="RPE and Choroid"  
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/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_1lb="UI-E-C11"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-C11 is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).  
TAG TISSUE=RPE and Choroid  
TAG LIB=UI-E-C11  
TAG\_SEQ=ACCTA"

## ORIGIN

Query Match 31.6%; Score 417; DB 5; Length 629;  
Best Local Similarity 100.0%; Pred. No. 5e-194;  
Matches 417, Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
905 TGCACCCCTCCAGCTTCGGAGACCCCGAGCAGCTGAACGACCGGAGTCGGTGGC 964  
Db TGCACCTTCAGCTTCGGAGACCCCGAGCAGCTGAACGACCGGAGTCGGTGGC 518  
965 GCACCCCAACAGAACCATCTTCAGCAGTGAACCTGATGATAGTCCAGGCTGGCGGC 1024  
Db GCACCCCAACAGAACCATCTTCAGCAGTGAACCTGATGATAGTCCAGGCTGGCGGC 458  
905 CCCTGCCCCCAGAGTAACTCGGGCATCAGCGCACTGCTACGGCAGCGCGGCGC 1084  
Db CCCTGCCCCCAGAGTAACTCGGGCATCAGCGCACTGCTACGGCAGCGCGGCGC 398  
905 ATGAGGGGGGGCGCGCCACCTACGAGGAGTCACTGCGCACTACCGGGGTCCTTC 1144  
Db ATGAGGGGGGGCGCGCCACCTACGAGGAGTCACTGCGCACTACCGGGGTCCTTC 338  
905 CAGCAGCAGCAGCAGTGGCGCGCTCTTGTCTGAGAGGGGACCCGCTCCACACACA 1204  
Db CAGCAGCAGCAGCAGTGGCGCGCTCTTGTCTGAGAGGGGACCCGCTCCACACACA 278  
905 CACATCGCGCCCTTAGAGAGCGCAGCATCTGAGCAAAAGAGAGATTAACAGAAAGA 1264  
Db CACATCGCGCCCTTAGAGAGCGCAGCATCTGAGCAAAAGAGAGATTAACAGAAAGA 218  
905 CACCTCTCTAGGGTCCCGAGGGGGGGCGGGCTGGGGCTGGTGTAGTAAAGGCGAG 1321  
Db CACCTCTCTAGGGTCCCGAGGGGGGGCGGGCTGGGGCTGGTGTAGTAAAGGCGAG 161

RESULT 34  
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LOCUS BMS59329  
DEFINITION AGNCOURT\_6598258 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5474455  
ACCESSION BMS59329  
VERSION BMS59329.1 GI:18802821

KEYWORDS  
SOURCE  
ORGANISM

EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 1400)  
NHI-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-rt@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: LICM1987 row: 1 column: 08  
High quality sequence stop: 462.

## FEATURES

Source

Location/Qualifiers

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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(C). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHI\_MGC library."

## ORIGIN

Query Match 30.7%; Score 406; DB 3; Length 1400;  
Best Local Similarity 99.8%; Pred. No. 1.3e-188;  
Matches 456, Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
83 GCTCGCTGGGGAAGCTAGGGGAGGCTCAGGCCCCCGGAGCGCGGCCGCTG 142  
Db 1 GCTCGCTGGGGAAGCTAGGGGAGGCTCAGGCCCCCGGAGCGCGGCCGCTG 60  
905 CCAAGCCATTTCGAGAGCGCACCGCGGCACTGCCAGCGCCCCCGGGCTGCCAGAG 202  
Db CCAAGCCATTTCGAGAGCGCACCGCGGCACTGCCAGCGCCCCCGGGCTGCCAGAG 120  
905 GAGGCGGGGGGGCGCAGCGGAGCGCGTCCCGGCACTAGAGCCCGCGCGCGGGA 262  
Db GAGGCGGGGGGGCGCAGCGGAGCGCGTCCCGGCACTAGAGCCCGCGCGCGGGA 180  
905 ACTTGGGGGGAACCGGAGCGCGGAGCGGGGGGGCGGCTCCCGCGGGCGCTCTG 322  
Db ACTTGGGGGGAACCGGAGCGCGGAGCGGGGGGGCGGCTCCCGCGGGCGCTCTG 240  
905 CATTGGGGGGCCCACTCCGGGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCC 382  
Db CATTGGGGGGCCCACTCCGGGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCC 300  
905 CGCGCCCGCC 442  
Db CGCGCCCGCC 360  
905 GCGCGCCCGCC 502  
Db GCGCGCCCGCC 420  
905 TTCAGAGCATGAGATCACGAGCTGAGTTTGTTC 539





FEATURES  
source

(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

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/dev\_stage="Adult and Fetal"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EC1"  
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site\_1: Ecor I; Site\_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGTCTAC.  
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383  
TAG LIB=UI-CF-EC1  
TAG\_SEQ=AAGTGTCTAC"

## ORIGIN

Query Match 30.2%; Score 399; DB 3; Length 626;  
Best Local Similarity 100.0%; Pred. No. 3.8e-185;  
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 923 GACCCGAGCAGCAGCTGAACTGAAACCGGAGTCGTGCGGCACCCCAAGAAACC 982  
Db 559 GACCCGAGCAGCAGCTGAACTGAAACCGGAGTCGTGCGGCACCCCAAGAAACC 500  
QY 983 ATCTTCGACAGTGAAGCTGATGATGATGACGAGCGGCGGCGCCCTGCCCCCAGCAGT 1042  
Db 499 ATCTTCGACAGTGAAGCTGATGATGATGACGAGCGGCGGCGCCCTGCCCCCAGCAGT 440  
QY 1043 AACTCGGAGCATCAGCGCAGCTGCTACCGGAGCGGCGGCATGAGAGGGCCGCGCCC 1102  
Db 439 AACTCGGAGCATCAGCGCAGCTGCTACCGGAGCGGCGGCATGAGAGGGCCGCGCCC 380  
QY 1103 ACTTACAGCGAGGTGATGCGCACTACCCGGGGGTCTCTCTTCAGCACCAGAGAGCAGT 1162  
Db 379 ACTTACAGCGAGGTGATGCGCACTACCCGGGGGTCTCTCTTCAGCACCAGAGAGCAGT 320  
QY 1163 GGGCGCGCTCTCTGCTGAGAGGGGACCGGGCTCCACACACACATGCGCGCCCTTAG 1222  
Db 319 GGGCGCGCTCTCTGCTGAGAGGGGACCGGGCTCCACACACACATGCGCGCCCTTAG 260  
QY 1223 AGCGAGCATCTGAGAGAAAGAGATTAACGAAAGACACCTCTTAGGGTCCC 1282  
Db 259 AGCGAGCATCTGAGAGAAAGAGATTAACGAAAGACACCTCTTAGGGTCCC 200  
QY 1283 CAGGGGGGCTGGGGCTGGCGTAGGTGAAGAGGAGC 1321  
Db 199 CAGGGGGGCTGGGGCTGGCGTAGGTGAAGAGGAGC 161

RESULT 37  
CN296134 544 bp mRNA linear EST 16-MAY-2004  
LOCUS CN296134  
DEFINITION 170006018766 GRN\_PRENNU Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN296134  
VERSION CN296134.1 GI:4312548

KEYWORDS  
SOURCE

EST.  
Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

## REFERENCE

1 (bases 1 to 544)

## AUTHORS

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G., J.,  
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,  
Ladkowski, J. and Stanton, L. W.

## TITLE

Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation

## JOURNAL

Nat. Biotechnol. 22 (6), 707-716 (2004)

## PUBMED

15146197

## COMMENT

Contact: Brandenberger R  
Regenerative Medicine  
Genon Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@genon.com  
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FEATURES  
source

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/note="Oligo dT primed, full-length enriched cDNA library  
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conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic acid and mitogens."

## ORIGIN

Query Match 29.9%; Score 395; DB 7; Length 544;  
Best Local Similarity 100.0%; Pred. No. 3.6e-183;  
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 CCGAGCAGCAGCTGGAAGTGAACCGGAGTCGTGCGGCACCCCAAGAAACATCT 986  
Db 9 CCGAGCAGCAGCTGGAAGTGAACCGGAGTCGTGCGGCACCCCAAGAAACATCT 68  
QY 987 TCAGCAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046  
Db 69 TCAGCAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 128  
QY 1047 CGGGCATCAGCGCCAGTGTCTACCGGAGCGGCGGCATGAGAGGGCCGCGCCACT 1106  
Db 129 CGGGCATCAGCGCCAGTGTCTACCGGAGCGGCGGCATGAGAGGGCCGCGCCACT 188  
QY 1107 ACAGCGAGGTGATGCGCACTACCCGGGGGTCTCTTCAGCACCAGAGAGAGTGGC 1166  
Db 189 ACAGCGAGGTGATGCGCACTACCCGGGGGTCTCTTCAGCACCAGAGAGAGTGGC 248  
QY 1167 CGCCCTCTCTGCTGAGAGGGGACCGGGCTCCACACACACATGCGCGCCCTTAGAGCG 1226  
Db 249 CGCCCTCTCTGCTGAGAGGGGACCGGGCTCCACACACACATGCGCGCCCTTAGAGCG 308  
QY 1227 CAGGCATCTGAGAGAAAGAGATTAACGAAAGACACCTCTTAGGGTCCCCAGG 1286  
Db 309 CAGGCATCTGAGAGAAAGAGATTAACGAAAGACACCTCTTAGGGTCCCCAGG 368  
QY 1287 GGGGCGGGGCTGGGGCTGGCGTAGGTGAAGAGGAGC 1321  
Db 369 GGGGCGGGGCTGGGGCTGGCGTAGGTGAAGAGGAGC 403

RESULT 38  
BUE83523 728 bp mRNA linear EST 07-OCT-2002  
LOCUS BUE83523/c  
DEFINITION UT-CF-EC1-accg-e-09-0-UI.81 UT-CF-EC1 Homo sapiens cDNA clone

ACCESSION BU683523  
 VERSION BU683523.1 GI:23535533  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 728)  
 AUTHORS Ronaldo M.F., Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@iowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=yes.  
 FEATURES  
 source  
 1..728  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-ECL1-acg-e-09-0-UI"  
 /tissue\_type="lung"  
 /dev\_stage="Adult and Fetal"  
 /lab\_host="PH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-ECL1"  
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-ECL1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTCTTAC.  
 TAG TISSUE=Normal Lung Epithelial Cells tissue nos 369-371 and 380-383  
 TAG LIB=UI-CF-ECL1  
 TAG\_SEQ=AAGTCTTAC"  
 ORIGIN  
 Query Match 29.8%; Score 393; DB 5; Length 728;  
 Best Local Similarity 99.8%; Pred. No. 3.4e-182;  
 Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 878 GAGAGACCCCTACCTACAGGAGCCCTTGCAGCTTCAGTGGAGACCCCGAGCAGC 937  
 DB 603 GAGAGACCCCTACCTACAGGAGCCCTTGCAGCTTCAGTGGAGACCCCGAGCAGC 544  
 QY 938 CTGGAACCTGAACCGGAGAGTCGGTGGCGGACCCCGAAGAGACCATCTTCGACAGTGC 997  
 DB 543 CTGGAACCTGAACCGGAGAGTCGGTGGCGGACCCCGAAGAGACCATCTTCGACAGTGC 484

QY 998 CTGATGATATGTGCACAGCTGGGCGGCCCTGCGCCCGCCAGCAGTAATCTGGGATGAGC 1057  
 DB 483 CTGATGATATGTGCACAGCTGGGCGGCCCTGCGCCCGCCAGCAGTAATCTGGGATGAGC 424  
 QY 1058 GCCACGTGTACACGACACGCGCGGCGCATGAGAGGCGCGCCCGCCTTACAGCGAGCTC 1117  
 DB 423 GCCACGTGTACAGTCAACGCGCGGCGCATGAGAGGCGCGCCCGCCTTACAGCGAGCTC 364  
 QY 1118 ATCGGCACTACCCGGGGTCTCTCTTCCAGACACAGAGACAGTGGCGGCGCTCTTG 1177  
 DB 363 ATCGGCACTACCCGGGGTCTCTCTTCCAGACACAGAGACAGTGGCGGCGCTCTTG 304  
 QY 1178 CTGAGGGGACCCGGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCATCTGG 1237  
 DB 303 CTGAGGGGACCCGGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCATCTGG 244  
 QY 1238 AGCAAGAGAGATTAACAGAAAGACACCTCTTAGAGGTCCTCCAGGGGGCGCGGCT 1297  
 DB 243 AGCAAGAGAGATTAACAGAAAGACACCTCTTAGAGGTCCTCCAGGGGGCGCGGCT 184  
 QY 1298 GGGGCTGCTAGTGTGAAAGGCGAG 1321  
 DB 183 GGGGCTGCTAGTGTGAAAGGCGAG 160  
 RESULT 39  
 BU169156 973 bp mRNA linear EST 04-SEP-2002  
 LOCUS AGENCOURT 7975486 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6082799  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BU169156  
 VERSION BU169156.1 GI:22683140  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 973)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA library preparation: Rubin Laboratory  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILMIL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILMIL at: http://image.llnl.gov  
 Plate: ILCM2311 row: 0 column: 24  
 High quality sequence stop: 500.  
 FEATURES  
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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6082799"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="PH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
 ORIGIN



AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaab8-rt@mail.nih.gov  
 CDNA Library Preparation:  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC)  
 Clone distribution: NCI-CCAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[info@llnl.gov](mailto:info@llnl.gov)  
 Plate: LLM8009 row: E column: 1  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

FEATURES  
source

```

1. 563
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3271656"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI-CCAP_P128"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP P122 was prepared, and 8
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615)."
Subtraction by Bento Soares and M. Fatima Bonaldo. "
```

## ORIGIN

Query Match 28.5%; Score 377; DB 6; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-174;  
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 945 TGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 1004
DB 10 TGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 69
QY 1005 ATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTGGGCACTACCGCCACGT 1064
DB 70 ATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTGGGCACTACCGCCACGT 129
QY 1065 GCTACGGCGAGCGGCGCGCATGAGAGGCGCGCCGCCCACTTACAGCGAGTCAATCGGCC 1124
DB 130 GCTACGGCGAGCGGCGCGCATGAGAGGCGCGCCGCCCACTTACAGCGAGTCAATCGGCC 189
QY 1125 ACTACCCCGGGGCTCTCTTCGACGACCGACAGAGTGGGCGCGCCCTTCCTTGTCTGGAGG 1184
DB 190 ACTACCCCGGGGCTCTCTTCGACGACCGACAGAGTGGGCGCGCCCTTCCTTGTCTGGAGG 249
QY 1185 GGACCCGGGCTTCACACACATCGCGCCCTTGAAGAGCGCAGCATCTTGAAGCAAG 1244
DB 250 GGACCCGGGCTTCACACACATCGCGCCCTTGAAGAGCGCAGCATCTTGAAGCAAG 309
QY 1245 AGAAGGATTAACAGAAAGACACCTCTCTGAGGGTCCCGAGGCGGCGGCTGGGGCTG 1304
DB 310 AGAAGGATTAACAGAAAGACACCTCTCTGAGGGTCCCGAGGCGGCGGCTGGGGCTG 369
QY 1305 CGTAGGTGAAAAGCGAG 1321
DB 370 CGTAGGTGAAAAGCGAG 386
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RESULT 42  
 LOCUS BMJ13900 552 bp mRNA linear EST 28-FEB-2002  
 DEFINITION UI-E-EJ0-abq-e-07-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

UI-E-EJ0-abq-e-07-0-UI.5', mRNA sequence.  
 BMJ13900  
 BMJ13900.1 GI:19027158  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

1 (bases 1 to 552)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 8893548  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 521-543, >POLY\_A#Simple\_repeat  
 Seq primer: M13 Reverse.

FEATURES  
source

```

1. 552
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-abq-e-07-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ0"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGAATCAAGA, lens, CGATTAGCCA, eye anterior segment,
AATCCCGCAT, optic nerve, CCATTATAGT, retina, CCGCG, Retina
foveal and Macular, GTCC, RPE and Choroid, ACTGA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI)."
```

## ORIGIN

Query Match 27.6%; Score 365; DB 3; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-168;  
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 944 CTGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 1003
DB 1 CTGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 60
QY 1004 GATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTGGGCACTACCGCCACG 1063
DB 61 GATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTGGGCACTACCGCCACG 120
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QY 1064 TGTCTACGGCAGCGCGCGGCGCATGTGAGAGGAGGCGCCGCCCACTTACAGAGAGTCAATCGGC 1123  
DB 121 TGTCTACGGCAGCGCGCGGCGCATGTGAGAGGAGGCGCCGCCCACTTACAGAGAGTCAATCGGC 180  
QY 1124 CACTACCGCGGGGCTCTCTTCTTCCAGACACAGAGAGAGTGGGCGCCCTCTTCTCTGAG 1183  
DB 181 CACTACCGCGGGGCTCTCTTCTTCCAGACACAGAGAGAGTGGGCGCCCTCTTCTCTGAG 240  
QY 1184 GGGAGCCGGGCTTCCACACACACATCGCGCCCTTACAGAGCGAGCCATCTGAGCAAA 1243  
DB 241 GGGAGCCGGGCTTCCACACACACATCGCGCCCTTACAGAGCGAGCCATCTGAGCAAA 300  
QY 1244 GAGAGAGTAAACAGAAAGAGACACCTTCTTACAGAGTCCCGGAGGCGCGCGCTTGGGCT 1303  
DB 301 GAGAGAGTAAACAGAAAGAGACACCTTCTTACAGAGTCCCGGAGGCGCGCGCTTGGGCT 360  
QY 1304 GCGTA 1308  
DB 361 GCGTA 365

RESULT 43  
BU174654 1127 bp mRNA linear EST 04-SEP-2002  
LOCUS BU174654  
DEFINITION AGENCOURT\_8045602 NIH\_MGC\_110 Homo sapiens CDNA clone IMAGE:6085305  
ACCESSION BU174654  
VERSION BU174654.1 GI:22688638  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 1127)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM2318 row: h column: 10  
High quality sequence start: 159  
High quality sequence stop: 554.  
Location/Qualifiers  
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/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1b="NIH MGC 110"  
/note="Organ: pancreas; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 27.1%; Score 358; DB 5; Length 1127;  
Best Local Similarity 99.8%; Pred. No. 6,2e-165;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 522 CGGAGCTGAGATTGTTCAAGTATCATCATGTGAGTGGTGGTGG 581  
DB 229 CGGAGCTGAGATTGTTCAAGTATCATCATGTGAGTGGTGGTGG 288  
QY 582 TGATCAAGTCCGTCTGAGGCACTACAGAGTGTCTGACAGTCTTCATCAGCGGACAC 641  
DB 289 TGATCAAGTCCGTCTGAGGCACTACAGAGTGTCTGACAGTCTTCATCAGCGGACAC 348  
QY 642 GCCAGGGGCGGAGAGAGAAAGATGCCCTGTCTCAAGAGATGCTGTGGCCCTCGGAGA 701  
DB 349 GCCAGGGGCGGAGAGAGAAAGATGCCCTGTCTCAAGAGATGCTGTGGCCCTCGGAGA 408  
QY 702 GCACAGTGTAGGCAACGGATATCCAGAGCGGAGGTTACAGCCCGGCGCCACCG 761  
DB 409 GCACAGTGTAGGCAACGGATATCCAGAGCGGAGGTTACAGCCCGGCGCCACCG 468  
QY 762 ACCGCTGCGCGTGGCGCCCTTCCAGCGGAGGCGCTTCCACCGCTTCCAGCGGAGCT 821  
DB 469 ACCGCTGCGCGTGGCGCCCTTCCAGCGGAGGCGCTTCCACCGCTTCCAGCGGAGCT 528  
QY 822 ATCCGTACTGACAGACAGAGATGACCTGCGACCCACCATCTGCTGACAGCGGAGG 881  
DB 529 ATCCGTACTGACAGACAGAGATGACCTGCGACCCACCATCTGCTGACAGCGGAGG 588  
QY 882 AGCCCCCAGCCCTACAGAGGCGCCCTGACACCTCAGAGTGGGAGCCCGGA 930  
DB 589 AGCCCCCAGCCCTACAGAGGCGCCCTGACACCTCAGAGTGGGAGCCCGGA 637

RESULT 44  
BU859841 646 bp mRNA linear EST 16-OCT-2002  
LOCUS BU859841  
DEFINITION AGENCOURT\_10442327 NIH\_MGC\_107 Homo sapiens CDNA clone  
IMAGE:6650815 5', mRNA sequence.  
ACCESSION BU859841  
VERSION BU859841.1 GI:24044833  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 646)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1CM2896 row: k column: 07  
High quality sequence stop: 551.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6650815"  
/tissue\_type="adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1b="NIH MGC 107"  
/note="Organ: breast; Vector: pORF7; Site\_1: EcoRI;  
Site\_2: XhoI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit









AI761441/c 693 bp mRNA linear EST 20-DEC-1999  
LOCUS  
DEFINITION  
W955f07.X1 Soares NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
IMAGE:2369989 3 similar to TR:015168 015168 CLONE 22. [3]  
TR:015167 TR:015165 ; mRNA sequence.  
ACCESSION  
AI761441  
VERSION  
AI761441.1 GI:5177108  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 693)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Unpublished (1997)  
Tumor Gene Index  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Insert Length: 1105 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 464.  
location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2369989"  
/lab\_host="MDH10B"  
/clone\_lib="Soares NSF\_F8\_9W\_OT\_PA\_P\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from five normalized  
libraries were mixed, and ss circles were made in vitro.  
Following HAP purification, this DNA was used as tracer in  
a subtractive hybridization reaction. The driver was  
PCR-amplified cDNAs from pools of 5,000 clones made from  
the same 5 libraries. The pools consisted of the following  
libraries and clones: Soares NBHSF pool 1:  
309384-310919, 323208-325895 Soares NB2HP pool 1:  
145032-147335, 147720-148103, 148872-149255, 15002 -  
150407, 151176-152327 Soares NB2HF8-9W pool 1:  
758280-760583, 772104-774407 Soares NBHPA pool 1:  
304776-306311, 320136-322823, 326280-326663 Soares NBHOT  
pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 22.9%; Score 302; DB 1; Length 693;  
Best Local Similarity 100.0%; Pred. No. 2.7e-137;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 885 CCCCACCTTACGAGGCCCCCTGCAACCTTCAGCTTCGGGACCCGAGAGCAGACTGGAAC 944  
DB 587 CCCCACCTTACGAGGCCCCCTGCAACCTTCAGCTTCGGGACCCGAGAGCAGACTGGAAC 528  
QY 945 TGAACCGGAGTGGGTGGCGGCACACCCCAACAAGCATCTTCAGACAGTGAAGCTGATGG 1004  
DB 527 TGAACCGGAGTGGGTGGCGGCACACCCCAACAAGCATCTTCAGACAGTGAAGCTGATGG 468  
QY 1005 ATAGTGCCAGGCTGGGGCGGCCCCCTGCCCCCAGAGTAACTCGGGCATCAGCGCACGT 1064  
DB 467 ATAGTGCCAGGCTGGGGCGGCCCCCTGCCCCCAGAGTAACTCGGGCATCAGCGCACGT 408  
QY 1065 GCTACGGGAGCGGGCGGCGATGAGGGGGCGGCCCACTACAGCGAGGTCACTGGGCC 1124  
DB 407 GCTACGGGAGCGGGCGGCGATGAGGGGGCGGCCCACTACAGCGAGGTCACTGGGCC 348  
QY 1125 ACTACCGGGGCTCTCTTCAGACAGCAGAGAGAGTGGGCGGCCCTTGTGCTGAGAGG 1184  
1 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
3 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 347 ACTACCGGGGCTCTCTTCAGACAGCAGAGAGAGTGGGCGGCCCTTGTGCTGAGAGG 288  
QY 1185 GG 1186  
DB 287 GG 286

Search completed: February 28, 2006, 11:47:21  
Job time : 5868 secs

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:09:56 ; Search time 275 Seconds  
(without alignments)  
8538,760 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321  
Sequence: 1 cgaccgcgcttcgagcga.....ctcgctaggtgaagaagcag 1321

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size: 23

Total number of hits satisfying chosen parameters: 354

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	800	60.6	1140 3	US-09-769-482-1
2	755	57.2	759 3	US-09-769-482-2
3	34	2.6	640 3	US-09-640-211A-146
4	31	2.3	359 3	US-09-640-211A-1198
5	31	2.3	533 3	US-09-640-211A-1340
6	31	2.3	2332 3	US-10-104-047-700
7	30	2.3	11729 3	US-09-949-016-13247
8	30	2.3	142783 3	US-09-949-016-15127
9	29	2.2	3430 3	US-09-949-016-1263
10	29	2.2	9406 3	US-09-949-016-13005
11	29	2.2	13892 3	US-09-949-016-17419
12	29	2.2	34230 3	US-09-949-016-12052
13	29	2.2	128470 3	US-09-949-016-13765
14	28	2.1	700 3	US-09-236-097-7
15	28	2.1	1203 3	US-09-086-010-1
16	28	2.1	1203 3	US-09-879-312A-1
17	28	2.1	3765 3	US-07-705-490-1
18	28	2.1	3765 3	US-07-751-891B-1
19	28	2.1	4362 2	US-08-455-073A-1
20	28	2.1	10348 2	US-08-457-273B-41
21	28	2.1	10348 2	US-08-556-419-13
22	28	2.1	10348 3	US-09-041-886-14
23	28	2.1	10366 2	US-08-246-982A-5
24	28	2.1	10366 2	US-08-453-265-5

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26	2.0	402	3	US-09-854-133-418	Sequence 418, App
27	2.0	8983	3	US-09-949-016-15437	Sequence 15437, A
28	2.0	154746	3	US-09-827-688-8	Sequence 8, App1
29	2.0	154746	3	US-09-827-688-8	Sequence 8, App1
30	2.0	367	3	US-09-325-932A-2	Sequence 2, App1
31	2.0	601	3	US-09-949-016-16860	Sequence 46860, A
32	2.0	641	3	US-09-436-699C-5	Sequence 5, App1
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34	2.0	1740	3	US-09-922-364A-15	Sequence 15, App1
35	2.0	1740	3	US-09-254-530-15	Sequence 15, App1
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63	1.9	457	2	US-08-332-766A-7	Sequence 7, App1
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71	1.9	22118	3	US-09-815-981A-5	Sequence 5, App1
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85	1.8	595	3	US-08-455-001-1	Sequence 1, App1
86	1.8	1809	2	US-08-393-465-1	Sequence 1, App1
87	1.8	1809	3	PCT-US95-11869-1	Sequence 1, App1
88	1.8	1809	6	US-09-854-133-430	Sequence 430, App
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90	1.8	2956	3	US-10-020-445A-89	Sequence 89, App1
91	1.8	3313	3	US-09-964-899-52	Sequence 52, App1
92	1.8	3313	3	US-09-949-016-13344	Sequence 13344, A
93	1.8	18079	3	US-10-283-247-3	Sequence 3, App1
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97	1.7	25	2	US-08-775-164-3	Sequence 3, App1

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120	23	1.7	69	3	US-08-484-408A-32	Sequence 32, Appl	193	23	1.7	2308	3	US-09-679-187-9	Sequence 9, Appli
121	23	1.7	78	3	US-09-573-080A-464	Sequence 464, App	194	23	1.7	2308	3	US-09-267-963D-9	Sequence 9, Appli
122	23	1.7	81	3	US-09-497-933A-24	Sequence 24, Appl	195	23	1.7	2308	3	US-09-949-016-657	Sequence 657, App
123	23	1.7	90	3	US-09-497-933A-20	Sequence 20, Appl	196	23	1.7	2400	3	US-10-104-047-228	Sequence 228, App
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125	23	1.7	103	3	US-09-513-999C-16230	Sequence 16230, A	198	23	1.7	2445	3	US-09-436-699E-21	Sequence 21, Appl
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249	23	1.7	4616	2	US-08-340-203A-1	Sequence 1, Appli	C 322	23	1.7	29686	3	US-09-949-016-16379	Sequence 16379, A
250	23	1.7	4616	2	US-08-452-567-1	Sequence 1, Appli	C 323	23	1.7	36389	3	US-09-949-016-15339	Sequence 15339, A
251	23	1.7	4616	2	US-08-452-427-1	Sequence 1, Appli	C 324	23	1.7	47284	3	US-09-949-016-17029	Sequence 17029, A
252	23	1.7	4616	2	US-09-085-407-1	Sequence 1, Appli	C 325	23	1.7	47375	3	US-09-949-016-15420	Sequence 15420, A
253	23	1.7	4724	3	US-09-949-016-681	Sequence 681, App	C 326	23	1.7	48794	3	US-09-949-016-15637	Sequence 15637, A
C 254	23	1.7	4951	3	US-09-949-016-5177	Sequence 5177, App	C 327	23	1.7	54382	3	US-09-949-016-12139	Sequence 12139, A
C 255	23	1.7	5011	2	US-08-141-893-1	Sequence 1, Appli	C 328	23	1.7	55195	3	US-09-949-016-15854	Sequence 15854, A
C 256	23	1.7	5011	2	US-08-463-092B-1	Sequence 1, Appli	C 329	23	1.7	60316	3	US-09-949-016-12423	Sequence 12423, A
C 257	23	1.7	5011	2	US-08-463-092B-3	Sequence 3, Appli	C 330	23	1.7	88758	3	US-09-949-016-13502	Sequence 13502, A
C 258	23	1.7	5011	2	US-08-462-109A-1	Sequence 1, Appli	C 331	23	1.7	91772	3	US-09-949-016-15568	Sequence 15568, A
C 259	23	1.7	5011	2	US-08-462-109A-3	Sequence 3, Appli	C 332	23	1.7	95255	3	US-09-949-016-17067	Sequence 17067, A
C 260	23	1.7	5011	2	US-08-460-907B-1	Sequence 1, Appli	C 333	23	1.7	110243	3	US-09-949-016-13698	Sequence 13698, A
C 261	23	1.7	5011	2	US-08-460-907B-3	Sequence 3, Appli	C 334	23	1.7	118067	3	US-09-949-016-13304	Sequence 13304, A
C 262	23	1.7	5011	2	US-08-463-179A-1	Sequence 1, Appli	C 335	23	1.7	120213	3	US-09-949-016-13304	Sequence 13304, A
C 263	23	1.7	5011	3	US-08-463-179A-3	Sequence 3, Appli	C 336	23	1.7	120217	3	US-09-949-016-12260	Sequence 12260, A
C 264	23	1.7	5011	3	US-08-461-384B-1	Sequence 1, Appli	C 337	23	1.7	133613	3	US-09-949-016-15824	Sequence 15824, A
C 265	23	1.7	5011	3	US-08-461-384B-3	Sequence 3, Appli	C 338	23	1.7	135687	3	US-09-949-016-15127	Sequence 15127, A
C 266	23	1.7	5011	3	US-08-407-207A-1	Sequence 1, Appli	C 339	23	1.7	142783	3	US-09-949-016-15127	Sequence 15127, A
C 267	23	1.7	5082	3	US-09-949-832C-18	Sequence 18, Appl	C 340	23	1.7	150597	3	US-09-949-016-15379	Sequence 15379, A
C 268	23	1.7	5202	3	US-09-949-016-1562	Sequence 1562, App	C 341	23	1.7	152393	3	US-09-949-016-14514	Sequence 14514, A
C 269	23	1.7	5222	3	US-07-751-891B-23	Sequence 23, Appl	C 342	23	1.7	152393	3	US-09-949-016-14515	Sequence 14515, A
C 270	23	1.7	5288	2	US-08-540-406-18	Sequence 18, Appl	C 343	23	1.7	153866	3	US-09-949-016-16219	Sequence 16219, A
C 271	23	1.7	5288	3	US-08-656-055-18	Sequence 18, Appl	C 344	23	1.7	156894	3	US-09-949-016-12765	Sequence 12765, A
C 272	23	1.7	5288	3	US-08-954-668-18	Sequence 18, Appl	C 345	23	1.7	156895	3	US-09-949-016-12766	Sequence 12766, A
C 273	23	1.7	5288	3	US-08-918-658-18	Sequence 18, Appl	C 346	23	1.7	156895	3	US-09-949-016-16957	Sequence 16957, A
C 274	23	1.7	5288	3	US-09-724-631-18	Sequence 18, Appl	C 347	23	1.7	156895	3	US-09-949-016-16958	Sequence 16958, A
C 275	23	1.7	5288	3	US-08-954-701A-18	Sequence 18, Appl	C 348	23	1.7	161652	3	US-09-949-016-15779	Sequence 15779, A
C 276	23	1.7	5288	3	US-09-754-032-18	Sequence 18, Appl	C 349	23	1.7	179905	3	US-09-949-016-12415	Sequence 12415, A
C 277	23	1.7	5288	6	PCR-US95-13233-18	Sequence 18, Appl	C 350	23	1.7	179905	3	US-09-949-016-12415	Sequence 12415, A
C 278	23	1.7	5482	3	US-09-470-443-3	Sequence 3, Appli	C 351	23	1.7	265038	3	US-09-949-016-12415	Sequence 12415, A
C 279	23	1.7	5482	3	US-09-397-550-19	Sequence 19, Appl	C 352	23	1.7	365032	3	US-09-949-016-15754	Sequence 15754, A
C 280	23	1.7	5482	3	US-09-635-872A-4	Sequence 4, Appli	C 353	23	1.7	365033	3	US-09-949-016-15754	Sequence 15754, A
C 281	23	1.7	5597	3	US-09-636-077A-4	Sequence 4, Appli	C 354	23	1.7	365033	3	US-09-949-016-15754	Sequence 15754, A
C 282	23	1.7	5597	3	US-09-636-060C-4	Sequence 4, Appli							
C 283	23	1.7	5597	3	US-09-986-552-4	Sequence 4, Appli							
C 284	23	1.7	5597	3	US-09-986-552-4	Sequence 4, Appli							
C 285	23	1.7	5597	3	US-10-023-888-3	Sequence 3, Appli							
C 286	23	1.7	5597	3	US-10-023-888-3	Sequence 3, Appli							
C 287	23	1.7	5597	3	US-10-306-686-4	Sequence 4, Appli							
C 288	23	1.7	5597	3	US-09-895-072-4	Sequence 4, Appli							
C 289	23	1.7	5597	3	US-10-023-888-3	Sequence 3, Appli							
C 290	23	1.7	6375	3	US-09-902-540-741	Sequence 741, App							
C 291	23	1.7	6721	3	US-09-949-016-518	Sequence 518, App							
C 292	23	1.7	7336	3	US-09-949-016-13935	Sequence 13935, A							
C 293	23	1.7	7460	3	US-09-949-016-13375	Sequence 13375, A							
C 294	23	1.7	7460	3	US-09-949-016-13384	Sequence 13384, A							
C 295	23	1.7	7700	3	US-09-949-016-15619	Sequence 15619, A							
C 296	23	1.7	7716	3	US-09-949-016-16614	Sequence 16614, A							
C 297	23	1.7	7890	3	US-09-949-016-11951	Sequence 11951, A							
C 298	23	1.7	7890	3	US-09-949-016-11956	Sequence 11956, A							
C 299	23	1.7	8831	3	US-09-949-016-17356	Sequence 17356, A							
C 300	23	1.7	9544	3	US-09-949-016-17608	Sequence 17608, A							
C 301	23	1.7	9592	2	US-08-393-734-3	Sequence 3, Appli							
C 302	23	1.7	9592	3	US-08-894-489-3	Sequence 3, Appli							
C 303	23	1.7	9592	3	US-10-167-264-3	Sequence 3, Appli							
C 304	23	1.7	10134	3	US-09-949-016-16668	Sequence 16668, A							
C 305	23	1.7	10304	3	US-09-627-465B-1	Sequence 1, Appli							
C 306	23	1.7	11003	3	US-09-949-016-13166	Sequence 13166, A							
C 307	23	1.7	11258	3	US-09-949-016-4037	Sequence 4037, App							
C 308	23	1.7	11580	3	US-09-334-220-4	Sequence 4, Appli							
C 309	23	1.7	12323	3	US-09-949-016-16703	Sequence 16703, A							
C 310	23	1.7	13290	3	US-09-949-016-13937	Sequence 13937, A							
C 311	23	1.7	13290	3	US-09-949-016-13938	Sequence 13938, A							
C 312	23	1.7	13316	3	US-09-949-016-14651	Sequence 14651, A							
C 313	23	1.7	14395	3	US-09-949-016-12247	Sequence 12247, A							
C 314	23	1.7	14395	3	US-09-949-016-16357	Sequence 16357, A							
C 315	23	1.7	15661	3	US-09-949-016-13161	Sequence 13161, A							
C 316	23	1.7	15695	3	US-09-949-016-15644	Sequence 15644, A							

## ALIGNMENTS

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RESULT 1
US-09-769-482-1
; Sequence 1, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOULI, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POUYNUCEOTIDE ARRAY
; FILE REFERENCE: 04995 0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(850)
US-09-769-482-1
Query Match 60.64; Score 800; DB 3; Length 1140;
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 2  
 US-09-769-482-2  
 ; Sequence 2, Application US/09769482  
 ; Patent No. 6566130  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SRIYASTAVA, SHIV  
 ; APPLICANT: MOUL, JUD D W.  
 ; APPLICANT: XU, LINDA L.  
 ; APPLICANT: SRGAWA, TAKAHIKO  
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED  
 ; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY  
 ; FILE REFERENCE: 04995.0057-00000  
 ; CURRENT APPLICATION NUMBER: US/09/769,482

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: CURRENT FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,772
: PRIOR FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/179,045
: PRIOR FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 67
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 759
: TYPE: DNA
: ORGANISM: Homo sapiens
:
US-09-769-482-2

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Query Match	57.2%	Score 755	DB 3	Length 759
Best Local Similarity	100.0%	Pred. No. 0		
Matches 755	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]

RESULT 3  
US-09-640-211A-146/C  
; Sequence 146, Application US/09640211A

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Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 146
LENGTH: 640
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-146

Query Match      2.3%; Score 31; DB 3; Length 640;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 78
DB      226 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 193

RESULT 4
US-09-640-211A-1198/C
Sequence 1198, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1198
LENGTH: 359
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-1198

Query Match      2.3%; Score 31; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
DB      206 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 176

RESULT 5
US-09-640-211A-1340/C
Sequence 1340, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
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NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1340
LENGTH: 533
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-1340

Query Match      2.3%; Score 31; DB 3; Length 533;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
DB      97 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 67

RESULT 6
US-10-104-047-700/C
Sequence 700, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
PRIOR FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 700
LENGTH: 2332
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-700

Query Match      2.3%; Score 31; DB 3; Length 2332;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
DB      1225 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 1195

RESULT 7
US-09-949-016-13247
Sequence 13247, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13247
LENGTH: 11729
TYPE: DNA
ORGANISM: Human
US-09-949-016-13247

Query Match      2.3%; Score 30; DB 3; Length 11729;
Best Local Similarity 100.0%; Pred. No. 0.0023;
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	Matches	30;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	45	GAGGAGGAGAGCGCGCGCGCGCGCG	74							
Db	10019	GAGGAGGAGAGCGCGCGCGCGCGCG	10048							

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      RESULT 8
US-09-949-016-15127
; Sequence 15127, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15127
; LENGTH: 142783
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(142783)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-949-016-15127

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RESULT 9
US-09-949-016-1263/c
; Sequence 1263; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1263
; LENGTH: 3430
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1263

Query Match          2.2%; Score 29; DB 3; Length 3430;
Best Local Similarity 100.0%; Pred. No. 0 0069;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
US-09-949-016-13005/c
? Sequence 13005, Application US/09949016
? Patent No. 6812339
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CLO01037
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13005
? LENGTH: 9406
? TYPE: DNA
? ORGANISM: Human
US-09-949-016-13005

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US-09-949-016-17419/c
; Sequence 17419, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17419
; LENGTH: 13832
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(13832)
; OTHER INFORMATION: n = A,T,C or G
;
US-09-949-016-17419

Query Match          2.2%; Score 29; DB 3; Length 13832;
Base Match Similarity 100.0%; Pred.No. 0.0061;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3765 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-07-751-891B-1

Query Match          2.1%; Score 28; DB 3; Length 3765;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches   28; Conservative    0; Mismatches     0; Indels    0; Gaps    0

Oy      56 GGCGGCGGGCGGGCGGCAGACGCC 83
Db      44 GGCGGCGGGCGGGCGGCAGACGCC 71

RESULT 19
US-08-455-073A-1
Sequence 1, Application US/08455073A
Patent No. 5876949
GENERAL INFORMATION:
APPLICANT: Gideon Dreyfuss
APPICANT: Mikko C. Siomi
APPLICANT: Van Zhang
TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
TITLE OF INVENTION: Of Making And Using The Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949rIs
STREET: One liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455, 073A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

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RESULT 21  
US-08-556-419-13/C  
Sequence 13, Application US/08556419C  
Patent No. 6093549  
GENERAL INFORMATION:  
APPLICANT: Ross, Christopher  
APPLICANT: Li, Xiao-Jiang  
APPLICANT: Li, Shi-Hua  
APPLICANT: Sharp, Alan  
APPLICANT: Lanahan, Anthony  
APPLICANT: Worley, Paul  
APPLICANT: Snyder, Solomon  
TITLE OF INVENTION: Huntingtin-associated protein  
FILE REFERENCE: 01107.52271  
CURRENT APPLICATION NUMBER: US/08/556.419C  
CURRENT FILING DATE: 1995-11-09  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 10348  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-556-419-13

Query Match 2.1%; Score 28; DB 3; Length 10348;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGCG 78  
Db 469 GAGGAGCGCGCGCGCGCGCGCGCG 442

RESULT 22  
US-09-041-886-14/C  
Sequence 14, Application US/09041886  
Patent No. 6235872  
GENERAL INFORMATION:  
APPLICANT: Bredesen, Dale E.  
APPLICANT: Rabizadeh, Shartoz  
TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
TITLE OF INVENTION: Polypeptides and Methods of Use  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041.886  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 2626  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10348 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

FEATURE:  
NAME/KEY: CDS  
LOCATION: 316..9748  
US-09-041-886-14

Query Match 2.1%; Score 28; DB 3; Length 10348;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGCG 78  
Db 469 GAGGAGCGCGCGCGCGCGCGCGCG 442

RESULT 23  
US-08-246-982A-5/C  
Sequence 5, Application US/08246982A  
Patent No. 5686288  
GENERAL INFORMATION:  
APPLICANT: Macdonald, Marcy E.  
APPLICANT: Ambrose, Christine M.  
APPLICANT: Duyao, Mabel P.  
APPLICANT: Gusella, James F.  
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/246.982A  
FILING DATE: May 20, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Joyce, A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0609.3880002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2540  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10366 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 316..9748  
US-08-246-982A-5

Query Match 2.1%; Score 28; DB 2; Length 10366;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGCG 78  
Db 469 GAGGAGCGCGCGCGCGCGCGCGCG 442

RESULT 24  
US-08-453-265-5/C  
Sequence 5, Application US/08453265  
Patent No. 5693757  
GENERAL INFORMATION:

APPLICANT: MacDonald, Marcy E.  
APPLICANT: Ambrose, Christine M.  
APPLICANT: Duyao, Mabel P.  
APPLICANT: Gussella, James F.  
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,265  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3880003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10366 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 316..9748  
US-08-453-265-5

Query Match 2.1%; Score 28; DB 2; Length 10366;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGAGAGCGCGCGCGCGCGCGCGCGCG 78  
DB 469 GAGAGAGCGCGCGCGCGCGCGCGCGCG 442

RESULT 25  
US-09-949-016-17589  
Sequence 17589, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17589  
LENGTH: 43117  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-17589

Query Match 2.1%; Score 28; DB 3; Length 43117;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 GCGCGCGCGCGCGCGCGCGCGCGCGCGCG 83  
DB 2083 GCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2110

RESULT 26  
US-09-854-133-418  
Sequence 418, Application US/09854133  
Patent No. 6759508  
GENERAL INFORMATION:  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Raedoh  
APPLICANT: Henderson, Robert A.  
APPLICANT: Benson, Darin R.  
APPLICANT: Secrist, Heather  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.475C10  
CURRENT APPLICATION NUMBER: US/09/854,133  
CURRENT FILING DATE: 2001-05-11  
NUMBER OF SEQ ID NOS: 735  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 418  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-854-133-418

Query Match 2.0%; Score 27; DB 3; Length 402;  
Best Local Similarity 100.0%; Pred. No. 0.06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGGAGAGCGCGCGCGCGCGCGCGCGCGCG 75  
DB 186 AGGAGAGCGCGCGCGCGCGCGCGCGCGCG 212

RESULT 27  
US-09-949-016-15437/C  
Sequence 15437, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15437  
LENGTH: 8983  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15437

Query Match 2.0%; Score 27; DB 3; Length 8983;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82

[illegible]



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LENGTH: 641
TYPE: DNA
ORGANISM: Triticum sp.
FEATURE:
NAME/KEY: unsure
LOCATION: (354)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (424)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (482)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (511)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (524)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (528)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (540)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (553)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (556)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (557)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (566)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (568)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (572)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (582)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (601)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (611)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (618)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure

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LOCATION: (623)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (641)
OTHER INFORMATION: n = a, c, g or t
US-09-436-699C-5

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Query Match 2.0%; Score 26; DB 3; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 56 GCGCGCGCGCGCGCGCGCGCGCGAGG 81
Db 66 GCGCGCGCGCGCGCGCGCGCGCGAGG 41

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RESULT 33
US-09-436-699C-19/c
Sequence 19, Application US/09436699C
Patent No. 6696619
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetases
FILE REFERENCE: B81266 US NA
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/107,276
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
LENGTH: 1719
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-436-699C-19

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Query Match 2.0%; Score 26; DB 3; Length 1719;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 56 GCGCGCGCGCGCGCGCGCGCGCGAGG 81
Db 66 GCGCGCGCGCGCGCGCGCGCGCGAGG 41

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RESULT 34
US-09-922-364A-15
Sequence 15, Application US/09922364A
Patent No. 6692937
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Maylie, James
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/922,364A  
FILING DATE: 03-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590  
FILING DATE: 10-Mar-1999  
APPLICATION NUMBER: US 60/026,451  
FILING DATE: 11-SEP-1996  
APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1740  
OTHER INFORMATION: /note= "rat small conductance,  
calcium-activated potassium channel  
protein 2 (rsk2) cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-922-364A-15

Query Match 2.0%; Score 26; DB 3; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGAGCGCGCGCGCGCGCGCGCG 78  
Db 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 35  
US-09-254-590-15  
Sequence 15, Application US/09254590  
Patent No. 6797486  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590  
FILING DATE: 10-Mar-1999

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,451  
FILING DATE: 11-SEP-1996  
APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1740  
OTHER INFORMATION: /note= "rat small conductance,  
calcium-activated potassium channel  
protein 2 (rsk2) cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-254-590-15

Query Match 2.0%; Score 26; DB 3; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGAGCGCGCGCGCGCGCGCGCG 78  
Db 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 36  
US-10-115-415-15  
Sequence 15, Application US/10115415  
Patent No. 6828122  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses  
Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/115,415  
FILING DATE: 02-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590

FILING DATE: 10-Mar-1999  
APPLICATION NUMBER: US 60/026,451  
FILING DATE: 11-SEP-1996  
APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1740  
OTHER INFORMATION: /note="rat small conductance,  
calcium-activated potassium channel  
protein 2 (rsk2) cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-115-415-15

Query Match 2.0%; Score 26; DB 3; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGCGCG 78  
DB 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 37  
US-10-116-260-15  
Sequence 15, Application US/10116260  
Patent No. 6828123  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses  
Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/116,260  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590  
FILING DATE: 10-Mar-1999

APPLICATION NUMBER: US 60/026,451  
FILING DATE: 11-SEP-1996  
APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1740  
OTHER INFORMATION: /note="rat small conductance,  
calcium-activated potassium channel  
protein 2 (rsk2) cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-116-260-15

Query Match 2.0%; Score 26; DB 3; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGCGCG 78  
DB 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 38  
US-10-115-671-15  
Sequence 15, Application US/10115671  
Patent No. 6828420  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses  
Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/115,671  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590  
FILING DATE: 10-Mar-1999  
APPLICATION NUMBER: US 60/026,451

FILED DATE: 11-SEP-1996  
APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1740  
OTHER INFORMATION: /note="rat small conductance,  
calcium-activated potassium channel  
protein 2 (rsk2) cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-115-671-15

Query Match 2.0%; Score 26; DB 3; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GAAGCGCGCGCGCGCGCGCGCG 78  
DB 262 GAAGCGCGCGCGCGCGCGCGCG 287

RESULT 39  
US-10-115-695-15  
Sequence 15, Application US/10115695  
Patent No. 6894147  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses  
Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/115,695  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590  
FILING DATE: 10-Mar-1999  
APPLICATION NUMBER: US 60/026,451  
FILING DATE: 11-SEP-1996

APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1740  
OTHER INFORMATION: /note="rat small conductance,  
calcium-activated potassium channel  
protein 2 (rsk2) cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-115-695-15

Query Match 2.0%; Score 26; DB 3; Length 1740;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GAAGCGCGCGCGCGCGCGCGCG 78  
DB 262 GAAGCGCGCGCGCGCGCGCGCG 287

RESULT 40  
US-09-780-173A-10  
Sequence 10, Application US/09780173A  
Patent No. 6455307  
GENERAL INFORMATION:  
APPLICANT: Robert McKay  
Applicant: Susan M. Freier  
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION  
FILE REFERENCE: RTS-0165  
CURRENT APPLICATION NUMBER: US/09/780,173A  
CURRENT FILING DATE: 2001-02-08  
NUMBER OF SEQ ID NOS: 95  
SEQ ID NO 10  
LENGTH: 1877  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (344)...(1396)  
US-09-780-173A-10

Query Match 2.0%; Score 26; DB 3; Length 1877;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 CCCC GCCCGCCGCCGCCGCCGCCGCC 405  
DB 278 CCCC GCCCGCCGCCGCCGCCGCCGCC 303

RESULT 41  
US-08-819-177-2/c  
Sequence 2, Application US/08819177  
Patent No. 6043083



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; APPLICANT: Bonny, Christopher
; TITLE OF INVENTION: Transcription Factor Islet Brain 1 (IB1)
; FILE REFERENCE: SJK/FP5805569
; CURRENT APPLICATION NUMBER: US/09/402,214
; CURRENT FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/GB98/00972
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: GB9706731.8
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: GB9709920.4
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2953
; TYPE: DNA
; ORGANISM: rattus
; US-09-402-214-1

Query Match      2.0%; Score 26; DB 3; Length 2953;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGGCGGCGGCGGCGGCGGCGG 78
DB 88 GGAGGCGGCGGCGGCGGCGGCGG 63

RESULT 45
US-09-949-016-1858/c
; Sequence 1858, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1858
; LENGTH: 2994
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1858

Query Match      2.0%; Score 26; DB 3; Length 2994;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGGCGGCGGCGGCGGCGG 76
DB 55 GAGGAGCGGCGGCGGCGGCGGCGG 30

RESULT 46
US-09-575-081B-7
; Sequence 7, Application US/09575081B
; Patent No. 6692934
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS
; FILE REFERENCE: DB23
; CURRENT APPLICATION NUMBER: US/09/575,081B
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/135,081
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; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 7
; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (713)..(713)
; OTHER INFORMATION: y = c or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2397)..(2397)
; OTHER INFORMATION: k = g or t
; US-09-575-081B-7

Query Match      2.0%; Score 26; DB 3; Length 3692;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGGCGGCGGCGGCGGCGGAG 81
DB 273 GCGCGCGGCGGCGGCGGCGGCGGAG 298

RESULT 47
US-09-799-451-260
; Sequence 260, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: PL_Fl_genes Version 2.0
; SEQ ID NO 260
; LENGTH: 3725
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (718)..(2778)
; US-09-799-451-260

Query Match      2.0%; Score 26; DB 3; Length 3725;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGGCGGCGGCGGCGGCGGAG 81
DB 374 GCGCGCGGCGGCGGCGGCGGCGGAG 399
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RESULT 48  
US-09-949-016-5656  
; Sequence 5656, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5656  
; LENGTH: 4412  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5656

Query Match 2.0%; Score 26; DB 3; Length 4412;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCGC 76  
DB 202 GAGGAGCGCGCGCGCGCGCGCGCGCGC 227

RESULT 49  
US-10-104-047-1017  
; Sequence 1017, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. 6943241el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1017  
; LENGTH: 4510  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-104-047-1017

Query Match 2.0%; Score 26; DB 3; Length 4510;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGGAGG 81  
DB 184 GCGCGCGCGCGCGCGCGCGCGCGGAGG 209

RESULT 50  
US-09-949-016-1137  
; Sequence 1137, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1137  
; LENGTH: 4714  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1137

Query Match 2.0%; Score 26; DB 3; Length 4714;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCGC 76  
DB 197 GAGGAGCGCGCGCGCGCGCGCGCGCGC 222

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Job time : 285 secs



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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:13:56 ; Search time 1202 Seconds  
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Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcgctctcgagcga.....ctgcgtagtgataaagcag 1321

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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	3	US-09-934-249-1
2	1229	93.0	4839	6	US-10-241-220-119
3	1229	93.0	4839	6	US-10-269-909-84
4	1229	93.0	4839	6	US-10-269-909-85
5	1229	93.0	4839	6	US-10-872-972-119
6	1229	93.0	4839	8	US-10-872-991-119
7	1229	93.0	4839	9	US-10-287-436A-300
8	864	65.2	864	6	US-10-295-027-127
9	861	65.2	861	3	US-09-934-249-3
10	800	60.6	1140	6	US-10-390-045-1
11	800	60.6	1140	7	US-10-434-479-1
12	800	60.6	1141	5	US-10-205-823-412
13	800	60.6	1141	6	US-10-301-822-208
14	800	60.6	1141	10	US-11-051-454-412
15	800	60.6	1850	6	US-10-241-220-44
16	800	60.6	1850	8	US-10-872-972-44
17	800	60.6	1850	8	US-10-872-991-44
18	800	60.6	4527	3	US-09-821-812-2
19	800	60.6	4527	8	US-10-849-635-2
20	788	59.7	1066	5	US-10-098-841-71
21	755	57.2	759	6	US-10-390-045-2
22	755	57.2	759	7	US-10-434-479-2
23	749	56.7	969	3	US-09-796-753-55

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26	713	54.0	806	8	US-10-872-991-45	Sequence 45, Appl
27	560	42.4	1583	5	US-10-000-266A-32	Sequence 32, Appl
28	401	32.9	693	3	US-09-934-249-14	Sequence 14, Appl
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30	178	13.5	1879	9	US-10-450-763-20307	Sequence 20307, A
31	106	8.0	368	3	US-09-783-590-3464	Sequence 3464, Ap
32	102	7.7	426	3	US-10-450-763-20306	Sequence 20306, A
33	63	4.8	426	3	US-09-908-975-13620	Sequence 13620, A
34	60	4.5	60	3	US-10-240-425-166	Sequence 166, App
35	56	4.2	522	7	US-09-783-590-3488	Sequence 3488, App
36	50	3.8	65	3	US-10-363-345A-30091	Sequence 30091, A
37	45	3.4	837	8	US-10-363-345A-30092	Sequence 30092, A
38	45	3.4	837	9	US-10-363-345A-30091	Sequence 30091, A
39	45	3.4	837	9	US-10-363-345A-30091	Sequence 30092, A
40	45	3.4	837	9	US-10-363-345A-30092	Sequence 30091, A
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46	37	2.8	837	9	US-10-363-345A-30089	Sequence 30090, A
47	37	2.8	837	9	US-10-363-345A-30090	Sequence 30090, A
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49	34	2.6	640	8	US-10-856-499-146	Sequence 146, App
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51	34	2.6	1752	7	US-10-437-963-48088	Sequence 48088, A
52	32	2.4	2000	7	US-10-260-238-2427	Sequence 2427, Ap
53	32	2.4	577	3	US-09-864-761-20542	Sequence 20542, A
54	32	2.4	630	7	US-10-437-963-45057	Sequence 45057, A
55	32	2.4	860	7	US-10-437-963-45057	Sequence 45057, A
56	32	2.4	1206	6	US-10-259-165-327	Sequence 327, App
57	32	2.4	1461	7	US-10-767-701-13778	Sequence 13778, A
58	32	2.4	1964	3	US-09-864-761-3776	Sequence 3776, Ap
59	31	2.3	231	7	US-10-437-963-93790	Sequence 93790, A
60	31	2.3	359	8	US-10-856-499-1198	Sequence 1198, Ap
61	31	2.3	533	8	US-10-856-499-1340	Sequence 1340, Ap
62	31	2.3	645	10	US-11-097-143-37082	Sequence 37082, A
63	31	2.3	776	8	US-10-363-345A-19999	Sequence 19999, A
64	31	2.3	776	9	US-10-363-345A-20000	Sequence 20000, A
65	31	2.3	776	9	US-10-363-345A-19999	Sequence 19999, A
66	31	2.3	934	9	US-10-363-345A-20000	Sequence 20000, A
67	31	2.3	934	9	US-10-767-701-9978	Sequence 9978, Ap
68	31	2.3	1295	7	US-10-437-963-11635	Sequence 11635, A
69	31	2.3	2332	6	US-10-104-047-700	Sequence 700, App
70	31	2.3	2808	10	US-11-097-143-37081	Sequence 37081, A
71	30	2.3	427	7	US-10-437-963-28554	Sequence 28554, A
72	30	2.3	918	7	US-10-437-963-28559	Sequence 28559, A
73	30	2.3	1750	7	US-10-437-963-28550	Sequence 28550, A
74	30	2.3	2109	9	US-10-450-763-11281	Sequence 11281, A
75	29	2.2	401	3	US-09-864-761-3536	Sequence 3536, Ap
76	29	2.2	446	3	US-09-864-761-20699	Sequence 20699, A
77	29	2.2	496	7	US-10-767-701-15679	Sequence 15679, A
78	29	2.2	543	7	US-10-437-963-70140	Sequence 70140, A
79	29	2.2	545	8	US-10-363-345A-29381	Sequence 29381, A
80	29	2.2	545	8	US-10-363-345A-29382	Sequence 29382, A
81	29	2.2	545	9	US-10-363-345A-29381	Sequence 29381, A
82	29	2.2	545	9	US-10-363-345A-29382	Sequence 29382, A
83	29	2.2	546	8	US-10-363-345A-12775	Sequence 12775, A
84	29	2.2	546	8	US-10-363-345A-12776	Sequence 12776, A
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103	29	2.2	1570	3	US-09-836-960-4	Sequence 4, Appl	176	28	2.1	2695	7	US-10-437-963-67083	Sequence 67083, A
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105	29	2.2	2253	7	US-10-437-963-17344	Sequence 17344, A	178	28	2.1	9732	9	US-10-450-763-15494	Sequence 15494, A
106	29	2.2	2322	7	US-10-112-944-42	Sequence 42, Appl	179	28	2.1	10348	7	US-10-276-774-427	Sequence 427, App
107	29	2.2	2482	7	US-10-450-763-21135	Sequence 21135, A	180	28	2.1	10348	7	US-10-276-774-490	Sequence 490, App
108	29	2.2	2608	8	US-10-482-029-282	Sequence 282, App	181	28	2.1	10348	7	US-10-419-997-2	Sequence 2, Appl
109	29	2.2	2853	3	US-09-905-983-45	Sequence 45, Appl	182	28	2.1	13672	6	US-10-450-763-27775	Sequence 27775, A
110	29	2.2	2853	6	US-10-177-293-42	Sequence 42, Appl	183	28	2.1	13672	6	US-10-172-118-727	Sequence 727, App
111	29	2.2	2853	7	US-10-778-146-5	Sequence 5, Appl	184	28	2.1	13994	7	US-10-342-887-127	Sequence 777, App
112	29	2.2	2859	6	US-10-437-963-74292	Sequence 74292, A	185	28	2.1	13994	7	US-10-721-693-9	Sequence 9, Appl
113	29	2.2	2987	6	US-10-017-621-89	Sequence 89, Appl	186	28	2.1	13994	6	US-10-811-455-114	Sequence 9, Appl
114	29	2.2	3131	8	US-10-723-860-2262	Sequence 2262, Ap	187	28	2.1	15698	6	US-10-367-094-108	Sequence 108, App
115	29	2.2	3131	9	US-10-756-149-2088	Sequence 2088, Ap	188	28	2.1	30611	7	US-10-367-094-108	Sequence 250, App
116	29	2.2	3266	3	US-09-814-353-20361	Sequence 20361, A	189	27	2.0	51	6	US-10-418-182-250	Sequence 61426, A
117	29	2.2	3444	6	US-10-293-582-16	Sequence 16, Appl	190	27	2.0	318	7	US-10-437-963-61426	Sequence 61426, A
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120	29	2.2	4122	8	US-10-159-563-31	Sequence 31, Appl	193	27	2.0	402	3	US-09-854-133-418	Sequence 418, App
121	29	2.2	4122	8	US-10-678-160A-13	Sequence 13, Appl	194	27	2.0	402	5	US-10-144-649A-418	Sequence 418, App
122	29	2.2	4136	9	US-10-450-763-14307	Sequence 14307, A	195	27	2.0	403	7	US-10-767-701-15176	Sequence 15176, A
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126	29	2.2	53828	7	US-10-322-281-369	Sequence 369, App	199	27	2.0	514	8	US-10-363-483A-19053	Sequence 19053, A
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128	29	2.2	1980090	8	US-10-741-600-17676	Sequence 17676, A	201	27	2.0	552	4	US-09-925-065A-373740	Sequence 373740, A
129	28	2.1	204	5	US-10-215-432-29	Sequence 29, Appl	202	27	2.0	557	7	US-10-424-599-137788	Sequence 137788, A
130	28	2.1	251	5	US-10-060-036-418	Sequence 418, App	203	27	2.0	581	8	US-10-363-345A-2401	Sequence 2401, Ap
131	28	2.1	293	7	US-10-437-963-57678	Sequence 57678, A	204	27	2.0	581	8	US-10-363-345A-2402	Sequence 2402, Ap
132	28	2.1	321	7	US-10-182-327-163	Sequence 163, App	205	27	2.0	581	9	US-10-363-483A-2401	Sequence 2401, Ap
133	28	2.1	354	7	US-10-437-963-46976	Sequence 46976, A	206	27	2.0	581	9	US-10-363-483A-2402	Sequence 2402, Ap
134	28	2.1	412	3	US-09-960-352-13161	Sequence 13161, A	207	27	2.0	583	4	US-09-925-065A-540849	Sequence 540849, A
135	28	2.1	496	3	US-09-783-590-3813	Sequence 3813, Ap	208	27	2.0	583	4	US-09-925-065A-540850	Sequence 540850, A
136	28	2.1	530	3	US-10-496-129-7	Sequence 7, Appl	209	27	2.0	598	7	US-10-303-165-13	Sequence 13, Appl
137	28	2.1	614	5	US-10-215-433-30	Sequence 30, Appl	210	27	2.0	598	9	US-10-983-197-13	Sequence 13, Appl
138	28	2.1	614	5	US-10-215-433-31	Sequence 31, Appl	211	27	2.0	598	10	US-11-004-765-13	Sequence 13, Appl
139	28	2.1	636	7	US-10-260-238-5871	Sequence 5871, Ap	212	27	2.0	615	9	US-10-487-901-3554	Sequence 3554, Ap
140	28	2.1	729	8	US-10-363-345A-19401	Sequence 19401, A	213	27	2.0	615	9	US-10-437-963-33920	Sequence 33920, A
141	28	2.1	729	8	US-10-363-345A-19402	Sequence 19402, A	214	27	2.0	820	9	US-10-487-901-4655	Sequence 4656, Ap
142	28	2.1	729	9	US-10-363-483A-19401	Sequence 19401, A	215	27	2.0	820	9	US-10-487-901-4655	Sequence 7235, Ap
143	28	2.1	729	9	US-10-363-483A-19402	Sequence 19402, A	216	27	2.0	838	7	US-10-437-963-8737	Sequence 8737, Ap
144	28	2.1	768	8	US-10-389-432B-41	Sequence 41, Appl	217	27	2.0	840	8	US-10-425-115-59262	Sequence 33262, A
145	28	2.1	768	8	US-10-389-432B-47	Sequence 47, Appl	218	27	2.0	849	7	US-10-437-963-17424	Sequence 17424, A
146	28	2.1	771	8	US-10-389-432B-37	Sequence 37, Appl	219	27	2.0	891	7	US-10-437-963-8727	Sequence 48727, A
147	28	2.1	771	8	US-10-389-432B-63	Sequence 63, Appl	220	27	2.0	900	9	US-10-450-763-23585	Sequence 23585, A
148	28	2.1	771	9	US-10-692-367-41	Sequence 41, Appl	221	27	2.0	948	7	US-10-437-963-17422	Sequence 17422, A
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150	28	2.1	774	8	US-10-389-432B-3	Sequence 3, Appl	223	27	2.0	1119	9	US-10-437-963-85098	Sequence 85098, A
151	28	2.1	774	9	US-10-692-367-7	Sequence 7, Appl	224	27	2.0	1119	9	US-10-481-032A-315	Sequence 315, App
152	28	2.1	774	9	US-10-692-367-37	Sequence 37, Appl	225	27	2.0	1119	9	US-10-481-080-16	Sequence 16, Appl
153	28	2.1	774	9	US-10-692-367-63	Sequence 63, Appl	226	27	2.0	1137	7	US-10-437-963-10547	Sequence 10547, A
154	28	2.1	777	9	US-10-692-367-3	Sequence 3, Appl	227	27	2.0	1137	7	US-10-437-963-10626	Sequence 10626, A
155	28	2.1	816	6	US-10-767-701-13440	Sequence 13440, A	228	27	2.0	1161	7	US-10-303-165-12	Sequence 12, Appl
156	28	2.1	840	6	US-10-259-165-762	Sequence 762, App	229	27	2.0	1161	7	US-10-983-197-12	Sequence 12, Appl
157	28	2.1	845	8	US-10-389-432B-7	Sequence 7, Appl	230	27	2.0	1161	10	US-11-004-765-12	Sequence 12, Appl
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159	28	2.1	1077	7	US-10-425-114-15467	Sequence 15467, A	232	27	2.0	1197	8	US-10-425-115-96876	Sequence 96876, A
160	28	2.1	1080	5	US-10-215-433-26	Sequence 26, Appl	233	27	2.0	1200	7	US-10-437-963-10546	Sequence 10546, A
161	28	2.1	1106	7	US-10-425-114-23460	Sequence 23460, A	234	27	2.0	1227	7	US-10-437-963-10066	Sequence 10066, A
162	28	2.1	1138	7	US-10-425-114-23406	Sequence 23406, A	235	27	2.0	1285	7	US-10-437-963-88997	Sequence 38997, A
163	28	2.1	1138	7	US-10-425-114-30480	Sequence 30480, A	236	27	2.0	1290	7	US-10-437-963-33855	Sequence 33855, A
164	28	2.1	1143	7	US-10-437-963-85810	Sequence 85810, A	237	27	2.0	1355	7	US-10-437-963-95417	Sequence 95417, A
165	28	2.1	1203	3	US-09-888-370-1	Sequence 1, Appl	238	27	2.0	1403	5	US-10-098-811-280	Sequence 280, App
166	28	2.1	1203	3	US-09-879-312-1	Sequence 1, Appl	239	27	2.0	1416	7	US-10-437-963-33054	Sequence 33054, A
167	28	2.1	1203	8	US-10-923-520-1	Sequence 1, Appl	240	27	2.0	1587	7	US-10-276-774-1315	Sequence 1315, Ap
168	28	2.1	1249	7	US-10-437-963-7575	Sequence 7575, Ap	241	27	2.0	1708	7	US-10-437-963-58654	Sequence 58654, A
169	28	2.1	1354	7	US-10-437-963-95417	Sequence 95417, A	242	27	2.0	1722	7	US-10-437-963-57856	Sequence 57856, A

243	27	2.0	1885	7	US-10-437-963-10100	Sequence 30100, A	316	26	2.0	764	9	US-10-363-483A-16699	Sequence 16699, A
244	27	2.0	1907	7	US-10-437-963-64881	Sequence 64881, A	317	26	2.0	764	9	US-10-363-483A-16700	Sequence 16700, A
245	27	2.0	2031	9	US-10-764-420-948	Sequence 948, App	318	26	2.0	767	7	US-10-260-238-177	Sequence 177, App
246	27	2.0	2424	7	US-10-437-963-62439	Sequence 62439, A	319	26	2.0	772	7	US-10-437-963-64300	Sequence 64300, A
247	27	2.0	2498	6	US-10-094-749-769	Sequence 769, App	320	26	2.0	776	8	US-10-425-115-114213	Sequence 114213, A
248	27	2.0	3110	9	US-10-887-553A-405	Sequence 405, App	321	26	2.0	776	8	US-10-363-445A-4157	Sequence 4157, App
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253	27	2.0	154746	3	US-09-827-688-8	Sequence 8, Appl	326	26	2.0	821	7	US-10-437-963-71107	Sequence 71107, A
254	27	2.0	154746	3	US-09-827-688-8	Sequence 8, Appl	327	26	2.0	827	7	US-10-437-963-701-936	Sequence 936, App
255	27	2.0	721377	9	US-10-461-862-163	Sequence 163, App	328	26	2.0	837	7	US-10-437-963-96070	Sequence 96070, A
256	27	2.0	171	5	US-10-062-727-5	Sequence 5, Appl	329	26	2.0	854	8	US-10-363-445A-17765	Sequence 17765, A
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258	26	2.0	267	7	US-10-437-963-90333	Sequence 90333, A	331	26	2.0	854	9	US-10-363-483A-17765	Sequence 17765, A
259	26	2.0	276	7	US-10-437-963-89331	Sequence 89331, A	332	26	2.0	854	9	US-10-437-963-17766	Sequence 17766, A
260	26	2.0	296	7	US-10-437-963-82869	Sequence 82869, A	333	26	2.0	866	9	US-10-437-963-16721	Sequence 16721, A
261	26	2.0	318	5	US-10-062-727-143	Sequence 143, App	334	26	2.0	909	8	US-10-363-445A-14665	Sequence 14665, A
262	26	2.0	367	5	US-10-219-220-2	Sequence 2, Appl	335	26	2.0	909	9	US-10-363-483A-14665	Sequence 14665, A
263	26	2.0	375	3	US-09-867-701-3254	Sequence 3254, App	336	26	2.0	909	9	US-10-363-483A-14666	Sequence 14666, A
264	26	2.0	386	7	US-10-424-559-16581	Sequence 16581, A	337	26	2.0	918	7	US-10-437-963-88734	Sequence 88734, A
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276	26	2.0	564	7	US-10-437-963-61188	Sequence 61188, A	349	26	2.0	1168	8	US-10-363-345A-33621	Sequence 33621, A
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281	26	2.0	581	8	US-10-363-345A-2472	Sequence 2472, App	354	26	2.0	1223	6	US-10-119-428-55	Sequence 55, Appl
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289	26	2.0	603	5	US-10-091-548-72	Sequence 72, Appl	362	26	2.0	1371	8	US-10-437-963-67047	Sequence 67047, A
290	26	2.0	603	5	US-10-074-095-600	Sequence 600, App	363	26	2.0	1393	7	US-10-739-930-2427	Sequence 2427, App
291	26	2.0	603	6	US-10-212-872-600	Sequence 281, App	364	26	2.0	1405	7	US-10-437-963-1630	Sequence 1630, App
292	26	2.0	621	7	US-10-260-238-281	Sequence 5, Appl	365	26	2.0	1419	7	US-10-437-963-88925	Sequence 88925, A
293	26	2.0	641	6	US-10-454-199-5	Sequence 7127, App	366	26	2.0	1419	8	US-10-425-115-117414	Sequence 117414, A
294	26	2.0	642	7	US-10-437-963-7127	Sequence 7127, App	367	26	2.0	1493	6	US-10-029-386-25133	Sequence 25133, A
295	26	2.0	645	5	US-10-219-220-208	Sequence 208, App	368	26	2.0	1493	6	US-10-029-386-25133	Sequence 25133, A
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297	26	2.0	656	3	US-10-487-901-5411	Sequence 5411, App	370	26	2.0	1497	8	US-10-363-345A-8947	Sequence 8947, App
298	26	2.0	665	4	US-09-925-065A-499554	Sequence 499554, A	371	26	2.0	1497	8	US-10-363-345A-8948	Sequence 8948, App
299	26	2.0	698	7	US-10-767-701-14484	Sequence 14484, A	372	26	2.0	1497	8	US-10-363-483A-8948	Sequence 8948, App
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301	26	2.0	705	7	US-10-425-115-117382	Sequence 117382, A	374	26	2.0	1501	7	US-10-437-963-77894	Sequence 77894, A
302	26	2.0	718	8	US-10-363-345A-167	Sequence 167, App	375	26	2.0	1523	7	US-10-425-114-34042	Sequence 34042, A
303	26	2.0	718	8	US-10-363-345A-168	Sequence 168, App	376	26	2.0	1533	7	US-10-437-963-45625	Sequence 45625, A
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305	26	2.0	718	9	US-10-363-483A-168	Sequence 168, App	378	26	2.0	1559	9	US-10-773-446-9	Sequence 9, Appl
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310	26	2.0	753	9	US-10-363-483A-26297	Sequence 26297, A	383	26	2.0	1667	9	US-10-956-157-1399	Sequence 1399, App
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390	26	2.0	1740	5	US-10-115-671-15	Sequence 15, Appl	463	26	2.0	783062	8	US-10-461-862-166	Sequence 166, App
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392	26	2.0	1740	5	US-10-116-260-15	Sequence 15, Appl	465	25	1.9	186	7	US-10-260-238-5267	Sequence 5267, App
393	26	2.0	1740	5	US-10-115-688-15	Sequence 15, Appl	466	25	1.9	207	7	US-10-437-963-74761	Sequence 74761, A
394	26	2.0	1740	10	US-11-116-760-15	Sequence 15, Appl	467	25	1.9	240	7	US-10-437-963-19420	Sequence 19420, A
395	26	2.0	1742	7	US-10-425-114-26517	Sequence 26517, A	468	25	1.9	243	7	US-10-437-963-48675	Sequence 48675, A
396	26	2.0	1824	7	US-10-437-963-23414	Sequence 23414, A	469	25	1.9	256	8	US-10-425-115-129084	Sequence 129084, A
397	26	2.0	1835	6	US-10-108-260A-1551	Sequence 1551, Ap	470	25	1.9	260	7	US-10-437-963-81329	Sequence 81329, A
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399	26	2.0	2000	7	US-10-260-238-1913	Sequence 1913, Ap	472	25	1.9	298	3	US-09-983-965-5793	Sequence 5793, App
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402	26	2.0	2172	7	US-10-437-963-53368	Sequence 53368, A	475	25	1.9	356	3	US-09-732-627A-128	Sequence 128, App
403	26	2.0	2212	7	US-10-425-114-25826	Sequence 25826, A	476	25	1.9	374	7	US-10-425-114-18037	Sequence 18037, A
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416	26	2.0	2832	5	US-10-115-178-2	Sequence 2, Appl	489	25	1.9	451	3	US-09-864-664-3	Sequence 3, Appl
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420	26	2.0	3297	9	US-10-450-763-27241	Sequence 27241, A	493	25	1.9	470	3	US-09-864-761-571	Sequence 571, App
421	26	2.0	3330	7	US-10-437-963-53409	Sequence 53409, A	494	25	1.9	470	7	US-10-767-701-21062	Sequence 21062, A
422	26	2.0	3427	5	US-10-044-090-589	Sequence 589, App	495	25	1.9	488	7	US-10-767-701-5716	Sequence 5716, App
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424	26	2.0	3692	7	US-10-437-963-30040	Sequence 30040, A	497	25	1.9	495	7	US-10-437-963-60997	Sequence 60997, A
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430	26	2.0	4070	6	US-10-062-674-1879	Sequence 1879, Ap	; Sequence 1, Application US/09934249						
431	26	2.0	4132	8	US-10-723-860-3472	Sequence 3472, Ap	; Parent No. US20020115081A1						
432	26	2.0	4132	8	US-10-756-149-3294	Sequence 3294, Ap	GENERAL INFORMATION:						
433	26	2.0	4510	6	US-10-104-047-1017	Sequence 1017, Ap	; APPLICANT: Lee, Richard T.						
434	26	2.0	4725	9	US-10-450-763-12179	Sequence 12179, A	; APPLICANT: Landschultz, Katherine T.						
435	26	2.0	4739	3	US-09-954-531-586	Sequence 586, App	; APPLICANT: Tuti, Thomas G.						
436	26	2.0	4739	5	US-10-193-651-22	Sequence 22, Appl	; APPLICANT: Thompson, John F.						
437	26	2.0	4739	9	US-10-843-641A-1653	Sequence 1653, Ap	; APPLICANT: Kennedy, Scott P.						
438	26	2.0	4739	9	US-10-956-157-1226	Sequence 1226, Ap	; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS						
439	26	2.0	4756	9	US-10-450-763-20834	Sequence 20834, A	; FILE REFERENCE: P0738/7001/ERP/KA						
440	26	2.0	4775	9	US-10-450-763-12181	Sequence 12181, A	; CURRENT APPLICATION NUMBER: US/09/934,249						
441	26	2.0	5012	8	US-10-719-993-252	Sequence 252, App	; PRIOR FILING DATE: 2001-08-21						
442	26	2.0	5012	8	US-10-461-862-183	Sequence 183, App	; PRIOR APPLICATION NUMBER: US 60/227,159						
443	26	2.0	5099	8	US-10-719-993-285	Sequence 285, App	; PRIOR FILING DATE: 2000-08-22						
444	26	2.0	5099	8	US-10-461-862-179	Sequence 179, App	; NUMBER OF SEQ ID NOS: 17						
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446	26	2.0	5186	9	US-10-461-862-181	Sequence 181, App	; SEQ ID NO 1						
447	26	2.0	5795	9	US-10-450-763-20835	Sequence 20835, A	; LENGTH: 1321						
448	26	2.0	7733	3	US-09-860-670-159	Sequence 159, App	; TYPE: DNA						
449	26	2.0	7733	6	US-10-227-646-159	Sequence 159, App	; ORGANISM: Homo Sapiens						
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453	26	2.0	15923	7	US-10-221-613-89	Sequence 89, Appl	US-09-934-249-1						
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455	26	2.0	33675	3	US-10-974-559-2	Sequence 2, Appl							
456	26	2.0	109906	7	US-10-235-192A-31	Sequence 31, Appl							
457	26	2.0	191597	8	US-10-719-993-6802	Sequence 6802, Ap							
458	26	2.0	227968	8	US-10-723-860-1357	Sequence 1357, Ap							
459	26	2.0	352938	7	US-10-322-666-79	Sequence 79, Appl							
460	26	2.0	400660	8	US-10-388-838-68	Sequence 68, Appl							
461	26	2.0	4398924	5	US-10-087-192-454	Sequence 454, App							







Db 781 ACGGGAGAGACCCCACTCAAGAGGACCCCTGCACTTCCAGTGGGAGCCCGAGC 840  
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Db 1201 GGGCTGGGGCTGCTGAGGTGAAAGAGCAG 1229

## RESULT 4

US-10-269-909-85  
Sequence 85, Application US/10269909  
Publication No. US20030180747A1  
GENERAL INFORMATION:  
APPLICANT: HRUBAN, RALPH H.  
APPLICANT: ARGENTI, PEDRAM  
APPLICANT: IACOBUZIO-DONAHUE, CHRISTINE  
APPLICANT: MAITRA, ANIRBAN  
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES  
FILE REFERENCE: 58303(71699)  
CURRENT APPLICATION NUMBER: US/10/269,909  
CURRENT FILING DATE: 2003-10-11  
PRIOR APPLICATION NUMBER: 60/328,609  
PRIOR FILING DATE: 2001-10-11  
PRIOR APPLICATION NUMBER: 60/332,754  
PRIOR FILING DATE: 2001-11-19  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 85  
LENGTH: 4839  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-269-909-85

Query Match 93.0%; Score 1229; DB 6; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAGCGCAGAGGCTCAGCCCGGCGGCGAGCGCGCGCGCTGCGAGCCCAT 152  
Db 1 GGAAGCTAGCGCAGAGGCTCAGCCCGGCGGCGAGCGCGCGCGCTGCGAGCCCAT 60  
Qy 153 TTCCGAGCCCAACCCCGGCGCACTGCGGAGCGCCCGGCGGCTGCGAGGGAGGCGGCG 212  
Db 61 TTCCGAGCCCAACCCCGGCGCACTGCGGAGCGCCCGGCGGCTGCGAGGGAGGCGGCG 120  
Qy 213 GGGCGAGCGAGCGGCTGCGCGCACTGAGCCCGCGGCGCGCGGAACTTGGCGCGC 272  
Db 121 GGGCGAGCGAGCGGCTGCGCGCACTGAGCCCGCGGCGCGCGGAACTTGGCGCGC 180

Qy 273 GACCCAGACCCCGGAGCCCGGCGCGCTTCCCGCGCGCGCTTCTGATCGGCGC 332  
Db 181 GACCCAGACCCCGGAGCCCGGCGCGCTTCCCGCGCGCGCTTCTGATCGGCGC 240  
Qy 333 CCCAGCTTCGGGCGCGCGCGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGC 392  
Db 241 CCCAGCTTCGGGCGCGCGCGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGC 300  
Qy 393 GC 452  
Db 301 GC 360  
Qy 453 CCGC 512  
Db 361 CCGC 420  
Qy 513 TGAAGATCAAGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTGTGTGTGTGA 572  
Db 421 TGAAGATCAAGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTGTGTGTGTGA 480  
Qy 573 TGA 632  
Db 481 TGA 540  
Qy 633 GCGGCGACAGCGCGGCGGAGAGAGAGATGCGCTGTCTTCAAGAGATGCTGTGCG 692  
Db 541 GCGGCGACAGCGCGGCGGAGAGAGAGATGCGCTGTCTTCAAGAGATGCTGTGCG 600  
Qy 693 CCTGAGAGAGCAGTGTGAGGCAACGAGATCCAGAGCGCGAGGTCTTCAAGAGATGCTGTGCG 752  
Db 601 CCTGAGAGAGCAGTGTGAGGCAACGAGATCCAGAGCGCGAGGTCTTCAAGAGATGCTGTGCG 660  
Qy 753 GAGCCACAGACCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 812  
Db 661 GAGCCACAGACCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 720  
Qy 813 AGCCCACTTATCCGATCCTGAGCAGAGATGCACTTGCACACCACTTCTGTGTGAG 872  
Db 721 AGCCCACTTATCCGATCCTGAGCAGAGATGCACTTGCACACCACTTCTGTGTGAG 780  
Qy 873 ACGGAGAGAGCCCGCACCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 932  
Db 781 ACGGAGAGAGCCCGCACCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGC 840  
Qy 933 AGCAGCTGGAACCTGAACCGGAGTGTGCGCGACCCCAAGAACATCTTTCAGCA 992  
Db 841 AGCAGCTGGAACCTGAACCGGAGTGTGCGCGACCCCAAGAACATCTTTCAGCA 900  
Qy 993 GTGACCTGATGATGTGTCAGGCTGGGCGGCGCCCTGCGCCCGGAGTAACTCGGCA 1052  
Db 901 GTGACCTGATGATGTGTCAGGCTGGGCGGCGCCCTGCGCCCGGAGTAACTCGGCA 960  
Qy 1053 TCAGGCGCACGCTGCTACGCGCAGCGGCGGCGATGAGAGGCGCGCGCCCACTTACAGC 1112  
Db 961 TCAGGCGCACGCTGCTACGCGCAGCGGCGGCGATGAGAGGCGCGCGCCCACTTACAGC 1020  
Qy 1113 AGGTATCGGCGCACTACCGGCGGCTCTCTTCAGCAGCAGCAGAGAGTGGCGCGCT 1172  
Db 1021 AGGTATCGGCGCACTACCGGCGGCTCTCTTCAGCAGCAGCAGAGAGTGGCGCGCT 1080  
Qy 1173 CCTTGTGAGGAGGAGCCCGGCTTCACACACATGCGCCCTTAAAGAGCGAGCA 1232  
Db 1081 CCTTGTGAGGAGGAGCCCGGCTTCACACACATGCGCCCTTAAAGAGCGAGCA 1140  
Qy 1233 TCTGAGAGCAAGAGAGATTAACAAGAAAGACACCTCTCTAGGGGTCCCGAGGGGCGC 1292  
Db 1141 TCTGAGAGCAAGAGAGATTAACAAGAAAGACACCTCTCTAGGGGTCCCGAGGGGCGC 1200  
Qy 1293 GGGCTGGGGCTGCTGAGGTGAAAGAGCAG 1321  
Db 1201 GGGCTGGGGCTGCTGAGGTGAAAGAGCAG 1229



















Db 760 AGGGAGCCCGCTCCACACACACATCGCCCTTAGAGAGCGACCATCTGAGCA 819  
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGCGGAGCTGGG 1301  
Db 820 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGCGGAGCTGGG 879  
Qy 1302 CTGCGTAGTGAAAAGGCGAG 1321  
Db 880 CTGCGTAGTGAAAAGGCGAG 899

## RESULT 15

US-10-241-220-44  
Sequence 44, Application US/10241220  
Publication No. US20030148408A1  
GENERAL INFORMATION:  
APPLICANT: Frantz, Gretchen  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Phillips, Heidi  
APPLICANT: Polakis, Paul  
APPLICANT: Spencer, Susan  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wu, Thomas  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF TUMOR  
FILE REFERENCE: P5010R1-US  
CURRENT APPLICATION NUMBER: US/10/241,220  
CURRENT FILING DATE: 2002-12-13  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 44  
LENGTH: 1850  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-241-220-44

Query Match 60.6%; Score 800; DB 6; Length 1850;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGTATGTATGTGTGTG 581  
Db 100 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGTATGTATGTGTGTG 159  
Qy 582 TGATCAGTGTCTGTGAGCACTCAAGCTGTCTGACGAGCTTTCATCAGCGGACCA 641  
Db 160 TGATCAGTGTCTGTGAGCACTCAAGCTGTCTGACGAGCTTTCATCAGCGGACCA 219  
Qy 642 GCCAGGGGCGAGAGAGAGATGCTCTCTCAGAAAGATGCTGTGGCTTCGAGGA 701  
Db 220 GCCAGGGGCGAGAGAGATGCTCTCTCAGAAAGATGCTGTGGCTTCGAGGA 279  
Qy 702 GCAAGTGTCAAGCAAGAAATCCAGAGCGGCAAGTCTAGCCGCCCTCGGCCACCG 761  
Db 280 GCAAGTGTCAAGCAAGAAATCCAGAGCGGCAAGTCTAGCCGCCCTCGGCCACCG 339  
Qy 762 ACCGCTGGCGGTGCGCCCTTCCAGCGGAGGAGCTTCCAGCGCTTCCAGCCACT 821  
Db 340 ACCGCTGGCGGTGCGCCCTTCCAGCGGAGGAGCTTCCAGCGCTTCCAGCCACT 399  
Qy 822 ATCCGTACTGAGAGACAGATGCACTGCAACCCACCATCTCGTGTCAAGCGGAGG 881  
Db 400 ATCCGTACTGAGAGACAGATGCACTGCAACCCACCATCTCGTGTCAAGCGGAGG 459  
Qy 882 AGCCCCACCTTACCAAGGCGCTTCAAGCTTGGGAGACCCCGAGAGAGAGCTGG 941  
Db 460 AGCCCCACCTTACCAAGGCGCTTCAAGCTTGGGAGACCCCGAGAGAGAGCTGG 519  
Qy 942 AACTGAACCGAGAGTGTGTGGGAGACCCCAAGAGAGATCTTTCAGAGTGAAGCTGA 1001  
Db 520 AACTGAACCGAGAGTGTGTGGGAGACCCCAAGAGAGATCTTTCAGAGTGAAGCTGA 579

Qy 1002 TGAATAGTGCAGAGCTGGGCGGCGCCCTGCCCCCAGCAGTAACTCGGGGANTAGCGCCA 1061  
Db 580 TGAATAGTGCAGAGCTGGGCGGCGCCCTGCCCCCAGCAGTAACTCGGGGANTAGCGCCA 639  
Qy 1062 CGTGCTACGGCAGCGGCGGCGCATGAGAGGGGCGCGCCCACTTACAGAGAGTCAATCG 1121  
Db 640 CGTGCTACGGCAGCGGCGGCGCATGAGAGGGGCGCGCCCACTTACAGAGAGTCAATCG 699  
Qy 1122 GCCACTACCGGGGGTCTCTCTTCAGACACAGAGAGCAGTGGGCGGCTCTCTGCTGG 1181  
Db 700 GCCACTACCGGGGGTCTCTCTTCAGACACAGAGAGCAGTGGGCGGCTCTCTGCTGG 759  
Qy 1182 AGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGAGCATCTGAGCA 1241  
Db 760 AGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGAGCATCTGAGCA 819  
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGCGGAGCTGGG 1301  
Db 820 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGCGGAGCTGGG 879  
Qy 1302 CTGCGTAGTGAAAAGGCGAG 1321  
Db 880 CTGCGTAGTGAAAAGGCGAG 899

## RESULT 16

US-10-872-972-44  
Sequence 44, Application US/10872972  
Publication No. US20040229277A1  
GENERAL INFORMATION:  
APPLICANT: Frantz, Gretchen  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Phillips, Heidi  
APPLICANT: Polakis, Paul  
APPLICANT: Spencer, Susan  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wu, Thomas  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF TUMOR  
FILE REFERENCE: P5010R1-US  
CURRENT APPLICATION NUMBER: US/10/872,972  
CURRENT FILING DATE: 2004-06-21  
PRIOR APPLICATION NUMBER: US/10/241,220  
PRIOR FILING DATE: 2002-09-11  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 44  
LENGTH: 1850  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-872-972-44

Query Match 60.6%; Score 800; DB 8; Length 1850;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGTATGTATGTGTGTG 581  
Db 100 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGTATGTATGTGTGTG 159  
Qy 582 TGATCAGTGTCTGTGAGCACTCAAGCTGTCTGACGAGCTTTCATCAGCGGACCA 641  
Db 160 TGATCAGTGTCTGTGAGCACTCAAGCTGTCTGACGAGCTTTCATCAGCGGACCA 219  
Qy 642 GCCAGGGGCGAGAGAGAGATGCTCTCTCAGAAAGATGCTGTGGCTTCGAGGA 701  
Db 220 GCCAGGGGCGAGAGAGAGATGCTCTCTCAGAAAGATGCTGTGGCTTCGAGGA 279  
Qy 702 GCAAGTGTCAAGCAAGAAATCCAGAGCGGCAAGTCTAGCCGCCCTCGGCCACCG 761  
Db 280 GCAAGTGTCAAGCAAGAAATCCAGAGCGGCAAGTCTAGCCGCCCTCGGCCACCG 339  
Qy 762 ACCGCTGGCGGTGCGCCCTTCCAGCGGAGGAGCTTCCAGCGCTTCCAGCCACT 821

Db 340 ACCGCTGACCGCTGCGCCCTTCCGCCACGCGGAGCGCTTCCACCGCTTCCAGCCCACT 399  
Qy 822 ATCCGTAAGTACGACGAGATGCACTGACCAACCACCATCTGCTGTGACAGCGGAGG 881  
Db 400 ATCCGTAAGTACGACGAGATGCACTGACCAACCACCATCTGCTGTGACAGCGGAGG 459  
Qy 882 AGCCCCCACTTACGAGGCGCCCTGACCTTCAAGCTTGGGACCCCGAGAGCAAGCTGG 941  
Db 460 AGCCCCCACTTACGAGGCGCCCTGACCTTCAAGCTTGGGACCCCGAGAGCAAGCTGG 519  
Qy 942 AACTGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTGAAGTGAAGCTGA 1001  
Db 520 AACTGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTGAAGTGAAGCTGA 579  
Qy 1002 TGAATAGTCCAGGCTGGGCGGCGCCCTGACCCCAAGCAATCTGGGATCAAGCGCA 1061  
Db 580 TGAATAGTCCAGGCTGGGCGGCGCCCTGACCCCAAGCAATCTGGGATCAAGCGCA 639  
Qy 1062 CTGCTACGCGACGCGCGGCGCATGAGAGGCGCGCCCACTTACAGCGAGTCAATCG 1121  
Db 640 CTGCTACGCGACGCGCGGCGCATGAGAGGCGCGCCCACTTACAGCGAGTCAATCG 699  
Qy 1122 GCACTACCGGAGGCTCTCTTCCAGACAGAGAGAGTGGGCGCGCTCTTGTGCTGG 1181  
Db 700 GCACTACCGGAGGCTCTCTTCCAGACAGAGAGAGTGGGCGCGCTCTTGTGCTGG 759  
Qy 1182 AGGGAGCCCGGCTCCACCAACATCGCGCCCTTGAAGAGCGGAGCATCTTGAAGCA 1241  
Db 760 AGGGAGCCCGGCTCCACCAACATCGCGCCCTTGAAGAGCGGAGCATCTTGAAGCA 819  
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCAAGGAGGCGCGGCTGGGG 1301  
Db 820 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCAAGGAGGCGCGGCTGGGG 879  
Qy 1302 CTGCTAGGTGAAGAGGAG 1321  
Db 880 CTGCTAGGTGAAGAGGAG 899

## RESULT 17

US-10-872-991-44  
; Sequence 44, Application US/10872991  
; Publication No. US20040242860A1  
; GENERAL INFORMATION:  
; APPLICANT: Frantcz, Gretchen J.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Phillips, Heidi  
; APPLICANT: Polakis, Paul  
; APPLICANT: Spencer, Susan  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wu, Thomas  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5010R1-US  
; CURRENT APPLICATION NUMBER: US/10/872,991  
; CURRENT FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US/10/241,220  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 44  
; LENGTH: 1850  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-872-991-44

Query Match 60.6%; Score 800; DB 8; Length 1850;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 CGAGCTGAGTGTGTTACATCATCATCATGCTGGTGTGATGATGATGATGATGATG 581

Db 100 CGAGCTGAGTGTGTTACATCATCATCATGCTGGTGTGATGATGATGATGATGATG 159  
Qy 582 TGAATACGTGCTGTGAGCACTTACAGTGTGTGACAGGTCTTATACAGCGGAGCA 641  
Db 160 TGAATACGTGCTGTGAGCACTTACAGTGTGTGACAGGTCTTATACAGCGGAGCA 219  
Qy 642 GCCAGGGGCGGAGAGAGATGCTGTCTCAGAAAGATGCTGTGAGCTCTGAGAG 701  
Db 220 GCCAGGGGCGGAGAGAGATGCTGTCTCAGAAAGATGCTGTGAGCTCTGAGAG 279  
Qy 702 GCAAGTGTGAGCAACGAGATCCAGAGCCGAGGCTTACGCTCCGCTGGCCCAAG 761  
Db 280 GCAAGTGTGAGCAACGAGATCCAGAGCCGAGGCTTACGCTCCGCTGGCCCAAG 339  
Qy 762 ACCGCTGAGCGGCTGCTTGGCCCAAGGAGAGGCTTCCAGCCGCTTCCAGCCACT 821  
Db 340 ACCGCTGAGCGGCTGCTTGGCCCAAGGAGAGGCTTCCAGCCGCTTCCAGCCACT 399  
Qy 822 ATCCGTAAGTACGACGAGATGCACTGACCAACCATCTGCTGTGACAGCGGAGG 881  
Db 400 ATCCGTAAGTACGACGAGATGCACTGACCAACCATCTGCTGTGACAGCGGAGG 459  
Qy 882 AGCCCCCACTTACGAGGCGCCCTGACCTTCAAGCTTGGGACCCCGAGAGCAAGCTGG 941  
Db 460 AGCCCCCACTTACGAGGCGCCCTGACCTTCAAGCTTGGGACCCCGAGAGCAAGCTGG 519  
Qy 942 AACTGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTGAAGTGAAGCTGA 1001  
Db 520 AACTGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTGAAGTGAAGCTGA 579  
Qy 1002 TGAATAGTCCAGGCTGGGCGGCGCCCTGACCCCAAGCAATCTGGGATCAAGCGCA 1061  
Db 580 TGAATAGTCCAGGCTGGGCGGCGCCCTGACCCCAAGCAATCTGGGATCAAGCGCA 639  
Qy 1062 CTGCTACGCGACGCGCGGCGCATGAGAGGCGCGCCCACTTACAGCGAGTCAATCG 1121  
Db 640 CTGCTACGCGACGCGCGGCGCATGAGAGGCGCGCCCACTTACAGCGAGTCAATCG 699  
Qy 1122 GCACTACCGGAGGCTCTCTTCCAGACAGAGAGAGTGGGCGCGCTCTTGTGCTGG 1181  
Db 700 GCACTACCGGAGGCTCTCTTCCAGACAGAGAGAGTGGGCGCGCTCTTGTGCTGG 759  
Qy 1182 AGGGAGCCCGGCTCCACCAACATCGCGCCCTTGAAGAGCGGAGCATCTTGAAGCA 1241  
Db 760 AGGGAGCCCGGCTCCACCAACATCGCGCCCTTGAAGAGCGGAGCATCTTGAAGCA 819  
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCAAGGAGGCGCGGCTGGGG 1301  
Db 820 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCAAGGAGGCGCGGCTGGGG 879  
Qy 1302 CTGCTAGGTGAAGAGGAG 1321  
Db 880 CTGCTAGGTGAAGAGGAG 899

## RESULT 18

US-09-821-812-2  
; Sequence 2, Application US/09821812  
; Publication No. US20030166520A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Biaoyang  
; TITLE OF INVENTION: Androgen Regulated Prostate Specific  
; TITLE OF INVENTION: Nucleic Acids  
; FILE REFERENCE: P-1S 4373  
; CURRENT APPLICATION NUMBER: US/09/821,812  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 4527  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
FEATURE:











	Matches	763;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	522	CGAGCTGGAGATTGTTTCAGATCATCATCATCTGCTGTGTGTATGTATGTGTATGTGTGTGTG	581							
Db	37	CGAGCTGGAGATTGTTTCAGATCATCATCATCTGCTGTGTGTATGTATGTGTATGTGTGTGTG	96							
QY	582	TGATCAGGTGCTGTGTGAGCCATCAAGACTGTCTGCAAGGCTCTTCATCAAGCCGGACACA	641							
Db	97	TGATCAGGTGCTGTGTGAGCCATCAAGACTGTCTGCAAGGCTCTTCATCAAGCCGGACACA	156							
QY	642	GCCAGGGGCGAGGAGAGAGATGCTCTGTCTCTAGAAAGATGCTCTGTGGCCCTTGGAGA	701							
Db	157	GCCAGGGGCGAGGAGAGAGATGCTCTGTCTCTAGAAAGATGCTCTGTGGCCCTTGGAGA	216							
QY	702	GCAACGTGTCAAGGCAACGAAATCCAGAGCCGAGGTCTTAGCCCTCGCTTGGCCACCG	761							
Db	217	GCAACGTGTCAAGGCAACGAAATCCAGAGCCGAGGTCTTAGCCCTCGCTTGGCCACCG	276							
QY	762	ACCGCTGTGGCCGTGCGCCCTTGGCCAGCCGGAGCGCTTCACGCGCTTCAGCCCACT	821							
Db	277	ACCGCTGTGGCCGTGCGCCCTTGGCCAGCCGGAGCGCTTCACGCGCTTCAGCCCACT	336							
QY	822	ATCCGTCCTTCAGACAGAGATTCAGCTTGCCACCCACCATCTCGCTGTCAAGCGGGAGAG	881							
Db	337	ATCCGTCCTTCAGACAGAGATTCAGCTTGCCACCCACCATCTCGCTGTCAAGCGGGAGAG	396							
QY	882	AGCCGCCACCTTACCGAGGGCCCTTGCACCTTCAGCTTGTGGAGCCCGAGCAGACTGG	941							
Db	397	AGCCGCCACCTTACCGAGGGCCCTTGCACCTTCAGCTTGTGGAGCCCGAGCAGACTGG	456							
QY	942	AACTGAACCGGGAGTTCGTGTGCTGCGGCAACCCCAACGAACCATCTTTCAGACATGACTGA	1001							
Db	457	AACTGAACCGGGAGTTCGTGTGCTGCGGCAACCCCAACGAACCATCTTTCAGACATGACTGA	516							
QY	1002	TGATAGTGGCCAGAGCTGGGGCGGCCCTTGGCCCCCAGCAGTAACTCGGGCATCAAGCGCA	1061							
Db	517	TGATAGTGGCCAGAGCTGGGGCGGCCCTTGGCCCCCAGCAGTAACTCGGGCATCAAGCGCA	576							
QY	1062	CGTGTACGCGCAGCGCGCGGCGCATGAGAGGGCGCGCCGCACTTACAGCAGAGTCAATCG	1122							
Db	577	CGTGTACGCGCAGCGCGGCGCATGAGAGGGCGCGCCGCACTTACAGCAGAGTCAATCG	636							
QY	1122	GCCACTAACCCGGGGTCTCTTTCAGACACACAGACAGAGTGGGCGCCCTCTTGTCTGG	1181							
Db	637	GCCACTAACCCGGGGTCTCTTTCAGACACACAGACAGAGTGGGCGCGCCCTCTTGTCTGG	696							
QY	1182	AGGGGACCCGGCTCCACACACACACATGCGGCCCTTAGAGCGCAGGCATCTGGAGCA	1241							
Db	697	AGGGGACCCGGCTCCACACACACACATGCGGCCCTTAGAGAGCGCAGGCATCTGGAGCA	756							
QY	1242	AAGAGAGGATTAACAGAAAGACACCTCTTAGGGTCCCGAG	1285							
Db	757	AAGAGAGGATTAACAGAAAGACACCTCTTAGGGTCCCGAG	800							
RESULT 25										
US-10-872-972-45										
; Sequence 45, Application US/10872972										
; Publication NO. US20040229277A1										
; GENERAL INFORMATION:										
; APPLICANT: Frantz, Gretchen										
; APPLICANT: Hillan, Kenneth J.										
; APPLICANT: Phillips, Heidi										
; APPLICANT: Polakis, Paul										
; APPLICANT: Spencer, Susan										
; APPLICANT: Williams, P. Mickey										
; APPLICANT: Wu, Thomas										
; APPLICANT: Zhang, Zemin										
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND										
; TITLE OF INVENTION: TREATMENT OF TUMOR										

```

; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 45
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-972-45

```

Query Match	54.0%	Score 713;	DB 8;	Length 806;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 763; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

[illegible]



```

US-10-779-543-11658
Sequence 11658, Application US/10779543
Publication No. US20050227917A1

GENERAL INFORMATION:
APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
  TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT FILING DATE: 2004-02-12

PRIOR APPLICATION NUMBER: 10/076,555
PRIOR FILING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: 09/217,471
PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/066,755
PRIOR FILING DATE: 1997-12-23

PRIOR APPLICATION NUMBER: 60/080,664
PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: 60/105,234
PRIOR FILING DATE: 1998-10-21

PRIOR APPLICATION NUMBER: 09/297,648
PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: PCT/US99/01619
PRIOR FILING DATE: 1999-01-28

PRIOR APPLICATION NUMBER: 60/072,910
PRIOR FILING DATE: 1998-01-28

PRIOR APPLICATION NUMBER: 60/075,954
PRIOR FILING DATE: 1998-02-24

PRIOR APPLICATION NUMBER: 60/080,114
PRIOR FILING DATE: 1998-03-31

Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 23767

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11658

LENGTH: 408

TYPE: DNA

ORGANISM: Homo sapiens

US-10-779-543-11658

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;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO: 20306
;; LENGTH: 426
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIMILAR
;; LOCATION: (13)..(57)
;; OTHER INFORMATION: 93% homologous to Homo sapiens du718u7.1 (PMEPA1 protein (an
;; OTHER INFORMATION: androgen induced type 1b transmembrane protein)), accession numbe
;; OTHER INFORMATION: AL035541, Smith-Waterman Score=79.
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(426)
;; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-20306
```

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Query Match          4.8%; Score 63; DB 9; Length 426;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1259 AAGAGCACCTCTCTAGAGGTCCTCCAGGGGCGGGCTGCGGCTGCGTAGGTGAAAGG 1318
DB 43 AAGAGCACCTCTCTAGAGGTCCTCCAGGGGCGGGCTGCGGCTGCGTAGGTGAAAGG 102
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QY 1319 CAG 1321
DB 103 CAG 105
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RESULT 34

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US-09-908-975-13620
;; Sequence 13620, Application US/09908975
;; Publication No. US20030165843A1
;; GENERAL INFORMATION:
;; APPLICANT: SHOSHAN, Avi
;; APPLICANT: WASSERMAN, Alon
;; APPLICANT: MINTZ, Eli
;; APPLICANT: MINTZ, Liat
;; APPLICANT: FAIGER, Simchon
;; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
;; FILE REFERENCE: 36688-0005
;; CURRENT APPLICATION NUMBER: US/09/908,975
;; PRIOR FILING DATE: 2001-07-20
;; PRIOR APPLICATION NUMBER: US 60/287,724
;; PRIOR FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: US 60/221,607
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 32337
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 13620
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-908-975-13620
```

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Query Match          4.5%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1225 CGGAGCATCTGGAGCAAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCA 1284
DB 1 CGGAGCATCTGGAGCAAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCA 60
```

RESULT 35

```
US-10-240-425-166
;; Sequence 166, Application US/10240425
;; Publication No. US2004003502A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Amanda
;; APPLICANT: Boland, Joseph F.
;; APPLICANT: Lord, Reginald V.
;; APPLICANT: Alvarez, Chris
;; APPLICANT: Wetzel, Jon C.
;; APPLICANT: Scheer, Uwe
;; APPLICANT: Vockley, Joseph G.
;; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;; FILE REFERENCE: 44921-5026
;; CURRENT APPLICATION NUMBER: US/10/240,425
;; PRIOR FILING DATE: 2002-09-30
;; PRIOR APPLICATION NUMBER: PCT/US01/09847
;; PRIOR FILING DATE: 2001-03-28
;; PRIOR APPLICATION NUMBER: US 60/193,446
;; PRIOR FILING DATE: 2000-03-31
;; NUMBER OF SEQ ID NOS: 1588
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 166
;; LENGTH: 522
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US2004003502A1 AA535819
US-10-240-425-166
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Query Match          4.2%; Score 56; DB 7; Length 522;
Best Local Similarity 100.0%; Pred. No. 5.5e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1234 CTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGG 1289
DB 36 CTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGG 91
```

RESULT 36

```
US-09-783-590-3488
;; Sequence 3488, Application US/09783590
;; Patent No. US20020110850A1
;; GENERAL INFORMATION:
;; APPLICANT: Dillon, Patrick J.
;; APPLICANT: Haseltine, William A.
;; APPLICANT: Li, Haodong
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Ruben, Steven M.
;; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
;; FILE REFERENCE: PO-16,2C1
;; CURRENT APPLICATION NUMBER: US/09/783,590
;; PRIOR FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: 08/420,856
;; PRIOR FILING DATE: 1995-04-12
;; PRIOR APPLICATION NUMBER: 08/346,731
;; PRIOR FILING DATE: 1994-11-21
;; NUMBER OF SEQ ID NOS: 12485
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 3488
;; LENGTH: 65
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (51)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3488
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Query Match          3.8%; Score 50; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1127 TACCGGGGTCTCTTCCAGACACAGAGAGAGTGGGCGCCCTCCT 1176  
Db 1 TACCGGGGTCTCTTCCAGACACAGAGAGAGTGGGCGCCCTCCT 50

RESULT 37  
US-10-363-345A-30091  
; Sequence 30091, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 30091  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-363-345A-30091

Query Match 3.4%; Score 45; DB 8; Length 837;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83  
Db 418 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 462

RESULT 38  
US-10-363-345A-30092/C  
; Sequence 30092, Application US/10363345A  
; Publication No. US20040234960A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Method for determining the degree of methylation of defined  
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3  
; FILE REFERENCE: E01/1227  
; CURRENT APPLICATION NUMBER: US/10/363,345A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 30092  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-Island No: 30092  
US-10-363-345A-30092

Query Match 3.4%; Score 45; DB 8; Length 837;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83  
Db 420 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 376

RESULT 39  
US-10-363-483A-30091  
; Sequence 30091, Application US/10363483A  
; Publication No. US20050064401A1

; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain  
; TITLE OF INVENTION: illnesses  
; FILE REFERENCE: 82011  
; CURRENT APPLICATION NUMBER: US/10/363,483A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 30091  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-Island No: 30091  
US-10-363-483A-30091

Query Match 3.4%; Score 45; DB 9; Length 837;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83  
Db 418 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 462

RESULT 40  
US-10-363-483A-30092/C  
; Sequence 30092, Application US/10363483A  
; Publication No. US20050064401A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain  
; TITLE OF INVENTION: illnesses  
; FILE REFERENCE: 82011  
; CURRENT APPLICATION NUMBER: US/10/363,483A  
; CURRENT FILING DATE: 2003-03-03  
; NUMBER OF SEQ ID NOS: 40712  
; SEQ ID NO 30092  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; OTHER INFORMATION: CpG-Island No: 30092  
US-10-363-483A-30092

Query Match 3.4%; Score 45; DB 9; Length 837;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83  
Db 420 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 376

RESULT 41  
US-09-934-249-12  
; Sequence 12, Application US/09934249  
; Patent No. US20020115081A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Richard T.  
; APPLICANT: Landschulz, Katherine T.  
; APPLICANT: Turi, Thomas G.  
; APPLICANT: Thompson, John F.  
; APPLICANT: Kennedy, Scott P.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS  
; FILE REFERENCE: P0738/7001/ERP/KA

CURRENT APPLICATION NUMBER: US/09/934,249  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/227,159  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 878  
TYPE: DNA  
ORGANISM: Mus Musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (20)...(841)  
US-09-934-249-12

Query Match 3.3%; Score 44; DB 3; Length 878;  
Best Local Similarity 100.0%; Pred.No. 4,2e-11;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 GGGGAGAGCCCCCAGCCCTACCAAGGGCCCTGACCTCCAGCT 918  
DB 458 GGGGAGAGCCCCCAGCCCTACCAAGGGCCCTGACCTCCAGCT 501

RESULT 42  
US-09-796-753-57  
Sequence 57, Application US/09/796,753  
Publication No. US20030027998A1  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-227-999  
CURRENT FILING DATE: US/09/796,753  
PRIOR APPLICATION NUMBER: 2001-03-01  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 09/223,094  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/223,546  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/224,246  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 09/259,388  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 60/122,458  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: 09/312,359  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/336,536  
PRIOR FILING DATE: 1999-06-18  
PRIOR APPLICATION NUMBER: 09/342,687  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 09/345,464  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: 09/365,164  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 09/399,723  
PRIOR FILING DATE: 1999-09-20  
PRIOR APPLICATION NUMBER: 09/409,634  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 09/471,179  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 09/474,071  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/474,072  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/514,010  
PRIOR FILING DATE: 2000-02-25  
PRIOR APPLICATION NUMBER: 09/516,745  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 09/572,002  
PRIOR FILING DATE: 2000-05-14  
PRIOR APPLICATION NUMBER: 09/597,993

PRIOR FILING DATE: 2000-06-19  
PRIOR APPLICATION NUMBER: 09/599,596  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 09/630,334  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: 09/606,565  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/606,317  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 09/665,666  
PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: 09/677,751  
PRIOR FILING DATE: 2000-09-30  
NUMBER OF SEQ ID NOS: 162  
SEQ ID NO 57  
LENGTH: 1713  
TYPE: DNA  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)...(652)  
US-09-796-753-57

Query Match 3.3%; Score 44; DB 3; Length 1713;  
Best Local Similarity 100.0%; Pred.No. 3,8e-11;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 GGGGAGAGCCCCCAGCCCTACCAAGGGCCCTGACCTCCAGCT 918  
DB 269 GGGGAGAGCCCCCAGCCCTACCAAGGGCCCTGACCTCCAGCT 312

RESULT 43  
US-09-934-249-15  
Sequence 15, Application US/09/934,249  
Patent No. US20020115081A1  
GENERAL INFORMATION:  
APPLICANT: Lee, Richard T.  
APPLICANT: Landeshultz, Katherine T.  
APPLICANT: Turti, Thomas G.  
APPLICANT: Thompson, John F.  
APPLICANT: Kennedy, Scott P.  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
FILE REFERENCE: P0738/7001/ERP/KA  
CURRENT FILING DATE: US/09/934,249  
PRIOR APPLICATION NUMBER: 2001-08-21  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 475  
TYPE: DNA  
ORGANISM: Mus Musculus  
US-09-934-249-15

Query Match 3.1%; Score 41; DB 3; Length 475;  
Best Local Similarity 100.0%; Pred.No. 1,4e-09;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 GCACCGCGCGCGCGCGCGCGGAGGAGCCCATGCTCTGCG 478  
DB 33 GCACCGCGCGCGCGCGCGCGGAGGAGCCCATGCTCTGCG 73

RESULT 44  
US-10-363-345A-30089/C  
Sequence 30089, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock





US-10-425-115-66221

Query Match 2.6%; Score 34; DB 8; Length 555;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 78  
DB 387 GAGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 420

RESULT 49

US-10-856-499-146/c  
; Sequence 146, Application US/10856499  
; Publication No. US20040259145A1  
; GENERAL INFORMATION:

APPLICANT: Shenk, Michael A.  
APPLICANT: Wood, Marion  
APPLICANT: McGrath, Anneette  
APPLICANT: Glenn, Matthew  
TITLE OF INVENTION: Compositions and Methods for the  
FILE REFERENCE: 11000.1021C2  
CURRENT APPLICATION NUMBER: US/10/856,499  
CURRENT FILING DATE: 2004-05-28  
NUMBER OF SEQ ID NOS: 2370  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 146  
LENGTH: 640  
TYPE: DNA  
ORGANISM: Eucalyptus grandis  
US-10-856-499-146

Query Match 2.6%; Score 34; DB 8; Length 640;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 78  
DB 226 GAGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 193

RESULT 50

US-10-739-930-3690/c  
; Sequence 3690, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:

APPLICANT: Kovacic, David K.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
FILE REFERENCE: 38-21(53377)B  
CURRENT APPLICATION NUMBER: US/10/739,930  
CURRENT FILING DATE: 2003-12-18  
NUMBER OF SEQ ID NOS: 11088  
SEQ ID NO 3690  
LENGTH: 1050  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER54078\_1  
US-10-739-930-3690

Query Match 2.6%; Score 34; DB 8; Length 1050;  
Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 78  
DB 422 GAGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 389

Search completed: February 28, 2006, 11:19:01  
Job time : 1213 secs

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:21:55 ; Search time 481 Seconds  
(without alignments)  
5856.251 Million cell updates/sec

Title: US-09-934-249-1

Sequence: 1 cgaccgcggtctcgcgaagcga.....ctgcgtagtgtgaaaagcag 1321

Gapop 60.0 , Gapext 60.0

Searched: 7209121 seqs, 1066183437 residues

word\_size : 23

Total number of hits satisfying chosen parameters: 351

Maximum DB seq length: 20000000000

Post-processing: Listing first 500 summaries

Database : Published Applications NA New: \*

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- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB\_seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB\_seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB\_seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB\_seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB\_seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB\_seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB\_seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB\_seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB\_seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	800	60.6	1141	12	US-11-186-284-208	Sequence 208, App
2	128	9.7	129	8	US-10-110-914A-7163	Sequence 7163, Ap
3	97	7.3	97	8	US-10-110-914A-6542	Sequence 6542, Ap
4	79	6.0	94	8	US-10-110-914A-1106	Sequence 1106, Ap
5	72	5.5	97	8	US-10-110-914A-1107	Sequence 1107, Ap
6	51	3.9	63	8	US-10-110-914A-7162	Sequence 7162, Ap
7	31	2.3	2352	9	US-11-072-512-700	Sequence 700, App
8	29	2.2	30	8	US-10-110-914A-399937	Sequence 399937, App
9	29	2.2	1546	10	US-11-112-944-14	Sequence 14, Appl
10	29	2.2	2947	8	US-11-136-527-114	Sequence 114, Appl
11	29	2.2	3131	8	US-10-770-726-28	Sequence 28, Appl
12	29	2.2	167891	12	US-11-121-086-14	Sequence 14, Appl
13	28	2.1	30	8	US-10-110-914A-100326	Sequence 100326, Appl
14	28	2.1	201	12	US-11-124-367A-4187	Sequence 4187, Ap
15	28	2.1	201	12	US-11-124-367A-4191	Sequence 4191, Ap
16	28	2.1	201	12	US-11-124-367A-4192	Sequence 4192, Ap
17	28	2.1	201	12	US-11-124-367A-4204	Sequence 4204, Ap
18	28	2.1	201	12	US-11-124-367A-4257	Sequence 4257, Ap
19	28	2.1	201	12	US-11-124-367A-4261	Sequence 4261, Ap
20	28	2.1	201	12	US-11-124-367A-4262	Sequence 4262, Ap

C 21	28	2.1	201	12	US-11-124-367A-437A	Sequence 437A, App
C 22	28	2.1	201	12	US-11-124-367A-4325	Sequence 4325, App
C 23	28	2.1	201	12	US-11-124-367A-4320	Sequence 4320, App
C 24	28	2.1	201	12	US-11-124-367A-4330	Sequence 4330, App
C 25	28	2.1	201	12	US-11-124-367A-4342	Sequence 4342, App
C 26	28	2.1	201	12	US-11-124-367A-4392	Sequence 4392, App
C 27	28	2.1	201	12	US-11-124-367A-4396	Sequence 4396, App
C 28	28	2.1	201	12	US-11-124-367A-4397	Sequence 4397, App
C 29	28	2.1	201	12	US-11-124-367A-4409	Sequence 4409, App
C 30	28	2.1	201	12	US-11-124-367A-2349A	Sequence 2349A, A
C 31	28	2.1	201	12	US-11-124-367A-23495	Sequence 23495, A
C 32	28	2.1	201	12	US-11-124-367A-23496	Sequence 23496, A
C 33	28	2.1	201	12	US-11-124-367A-23708	Sequence 23708, A
C 34	28	2.1	2097	12	US-11-024-959-254	Sequence 254, App
C 35	28	2.1	5453	12	US-11-136-527-3064	Sequence 3064, App
C 36	28	2.1	12200	12	US-11-124-367A-206	Sequence 206, App
C 37	28	2.1	12728	12	US-11-124-367A-207	Sequence 207, App
C 38	28	2.1	13643	12	US-11-124-367A-205	Sequence 204, App
C 39	28	2.1	13653	12	US-11-124-367A-205	Sequence 205, App
C 40	28	2.1	13672	12	US-11-055-035-2	Sequence 2, App11
C 41	27	2.0	110	8	US-10-310-914A-4814	Sequence 4814, Ap
C 42	27	2.0	110	8	US-10-310-914A-12873	Sequence 12873, A
C 43	27	2.0	110	8	US-10-310-914A-20511	Sequence 20511, A
C 44	27	2.0	552	6	US-09-925-065A-373740	Sequence 373740, A
C 45	27	2.0	583	6	US-09-925-065A-540849	Sequence 540849, A
C 46	27	2.0	583	6	US-09-925-065A-540850	Sequence 540850, A
C 47	26	2.0	665	6	US-09-925-065A-499554	Sequence 499554, A
C 48	26	2.0	1598	12	US-11-136-527-2759	Sequence 2759, App
C 49	26	2.0	2074	12	US-11-136-527-2522	Sequence 2522, App
C 50	26	2.0	2127	8	US-10-750-185-34757	Sequence 34757, A
C 51	26	2.0	2127	8	US-10-750-623-34757	Sequence 34757, A
C 52	26	2.0	2802	8	US-10-955-054A-97	Sequence 97, App1
C 53	26	2.0	4510	9	US-11-072-512-1017	Sequence 1017, Ap
C 54	26	2.0	4739	8	US-10-770-726-2	Sequence 2, App11
C 55	26	2.0	193363	12	US-11-112-908-32	Sequence 32, App1
C 56	25	1.9	25	8	US-10-310-914A-399898	Sequence 399898, A
C 57	25	1.9	25	12	US-11-121-849-216510	Sequence 216510, A
C 58	25	1.9	229	8	US-10-310-914A-298798	Sequence 298798, A
C 59	25	1.9	171	12	US-11-043-752-3725	Sequence 3725, App
C 60	25	1.9	294	12	US-11-043-752-3731	Sequence 3731, App
C 61	25	1.9	329	12	US-11-043-752-3738	Sequence 3728, App
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C 65	25	1.9	2961	9	US-11-072-512-428	Sequence 428, App
C 66	25	1.9	7028	12	US-11-043-752-39	Sequence 39, App
C 67	25	1.9	17384	12	US-11-082-154A-118	Sequence 118, App
C 68	25	1.9	22118	12	US-11-082-154A-18	Sequence 18, App1
C 69	25	1.9	79666	12	US-11-043-752-1	Sequence 1, App1
C 70	25	1.9	137000	8	US-10-515-538-11	Sequence 11, App1
C 71	25	1.9	217623	12	US-11-112-908-33	Sequence 33, App1
C 72	24	1.8	24	8	US-10-310-914A-27143	Sequence 27143, A
C 73	24	1.8	24	8	US-10-310-914A-100285	Sequence 27164, A
C 74	24	1.8	24	8	US-10-310-914A-100285	Sequence 100285, A
C 75	24	1.8	24	8	US-10-310-914A-156013	Sequence 100286, A
C 76	24	1.8	24	8	US-10-310-914A-156013	Sequence 156013, A
C 77	24	1.8	24	8	US-10-310-914A-163380	Sequence 163380, A
C 78	24	1.8	24	8	US-10-310-914A-167328	Sequence 167328, A
C 79	24	1.8	24	8	US-10-310-914A-167697	Sequence 167697, A
C 80	24	1.8	24	8	US-10-310-914A-167698	Sequence 167698, A
C 81	24	1.8	24	8	US-10-310-914A-182849	Sequence 182849, A
C 82	24	1.8	24	8	US-10-310-914A-298710	Sequence 298710, A
C 83	24	1.8	24	8	US-10-310-914A-399951	Sequence 399951, A
C 84	24	1.8	24	8	US-10-310-914A-432630	Sequence 432630, A
C 85	24	1.8	24	8	US-10-310-914A-536225	Sequence 536225, A
C 86	24	1.8	24	8	US-10-310-914A-576635	Sequence 576635, A
C 87	24	1.8	24	8	US-10-310-914A-707839	Sequence 707839, A
C 88	24	1.8	24	8	US-10-310-914A-875273	Sequence 875273, A
C 89	24	1.8	24	8	US-10-310-914A-899422	Sequence 899422, A
C 90	24	1.8	24	8	US-10-310-914A-972860	Sequence 972860, A
C 91	24	1.8	24	8	US-10-310-914A-1065872	Sequence 1065872, A
C 92	24	1.8	25	8	US-10-310-914A-156005	Sequence 156005, A
C 93	24	1.8	25	8	US-10-310-914A-875316	Sequence 875316, A

C 94	24	1.8	25	8	US-10-310-914A-1065870	Sequence 1065870,	C 167	23	1.7	23	8	US-10-310-914A-1065871	Sequence 1065871,
C 95	24	1.8	27	8	US-10-310-914A-432650	Sequence 432650,	C 168	23	1.7	24	8	US-10-310-914A-78097	Sequence 78097, A
C 96	24	1.8	29	8	US-10-310-914A-707883	Sequence 707883	C 169	23	1.7	24	8	US-10-310-914A-87752	Sequence 87752, A
C 97	24	1.8	520	12	US-11-123-896-373	Sequence 373, App	C 170	23	1.7	24	8	US-10-310-914A-94850	Sequence 94850, A
C 98	24	1.8	637	6	US-09-925-065A-887583	Sequence 887583,	C 171	23	1.7	24	8	US-10-310-914A-94851	Sequence 94851, A
C 99	24	1.8	637	6	US-09-925-065A-911994	Sequence 911994,	C 172	23	1.7	24	8	US-10-310-914A-94852	Sequence 94852, A
C 100	24	1.8	658	6	US-09-925-065A-883427	Sequence 883427,	C 173	23	1.7	24	8	US-10-310-914A-94853	Sequence 94853, A
C 101	24	1.8	836	7	US-09-925-065A-8376	Sequence 8376, Ap	C 174	23	1.7	24	8	US-10-310-914A-122968	Sequence 122968
C 102	24	1.8	855	7	US-10-714-887-127	Sequence 127, App	C 175	23	1.7	24	8	US-10-310-914A-163371	Sequence 163371,
C 103	24	1.8	1719	8	US-10-750-185-24932	Sequence 24932, A	C 176	23	1.7	24	8	US-10-310-914A-163372	Sequence 163372,
C 104	24	1.8	1719	8	US-10-750-623-24932	Sequence 24932, A	C 177	23	1.7	24	8	US-10-310-914A-163373	Sequence 163373,
C 105	24	1.8	3846	12	US-11-136-527-3312	Sequence 3312, Ap	C 178	23	1.7	24	8	US-10-310-914A-167690	Sequence 167690,
C 106	24	1.8	5801	12	US-11-000-463-580	Sequence 580, App	C 179	23	1.7	24	8	US-10-310-914A-167691	Sequence 167691,
C 107	24	1.8	153376	12	US-11-121-086-5	Sequence 5, Appl	C 180	23	1.7	24	8	US-10-310-914A-167692	Sequence 167692,
C 108	24	1.8	162013	12	US-11-150-888-30	Sequence 30, Appl	C 181	23	1.7	24	8	US-10-310-914A-167693	Sequence 167693,
C 109	24	1.8	172543	12	US-11-121-086-6	Sequence 6, Appl	C 182	23	1.7	24	8	US-10-310-914A-167694	Sequence 167694,
C 110	23	1.7	23	8	US-10-310-914A-42427	Sequence 42427, A	C 183	23	1.7	24	8	US-10-310-914A-167695	Sequence 167695,
C 111	23	1.7	23	8	US-10-310-914A-42428	Sequence 42428, A	C 184	23	1.7	24	8	US-10-310-914A-167696	Sequence 167696,
C 112	23	1.7	23	8	US-10-310-914A-42429	Sequence 42429, A	C 185	23	1.7	24	8	US-10-310-914A-167716	Sequence 167716,
C 113	23	1.7	23	8	US-10-310-914A-42430	Sequence 42430, A	C 186	23	1.7	24	8	US-10-310-914A-167717	Sequence 167717,
C 114	23	1.7	23	8	US-10-310-914A-42431	Sequence 42431, A	C 187	23	1.7	24	8	US-10-310-914A-189745	Sequence 189745,
C 115	23	1.7	23	8	US-10-310-914A-42432	Sequence 42432, A	C 188	23	1.7	24	8	US-10-310-914A-189746	Sequence 189746,
C 116	23	1.7	23	8	US-10-310-914A-42433	Sequence 42433, A	C 189	23	1.7	24	8	US-10-310-914A-189747	Sequence 189747,
C 117	23	1.7	23	8	US-10-310-914A-51709	Sequence 51709, A	C 190	23	1.7	24	8	US-10-310-914A-226067	Sequence 226067,
C 118	23	1.7	23	8	US-10-310-914A-78091	Sequence 78091, A	C 191	23	1.7	24	8	US-10-310-914A-255936	Sequence 255936,
C 119	23	1.7	23	8	US-10-310-914A-78092	Sequence 78092, A	C 192	23	1.7	24	8	US-10-310-914A-255937	Sequence 255937,
C 120	23	1.7	23	8	US-10-310-914A-88240	Sequence 88240, A	C 193	23	1.7	24	8	US-10-310-914A-280846	Sequence 280846,
C 121	23	1.7	23	8	US-10-310-914A-100311	Sequence 100311,	C 194	23	1.7	24	8	US-10-310-914A-317199	Sequence 317199,
C 122	23	1.7	23	8	US-10-310-914A-100329	Sequence 100329,	C 195	23	1.7	24	8	US-10-310-914A-317200	Sequence 317200,
C 123	23	1.7	23	8	US-10-310-914A-156012	Sequence 156012,	C 196	23	1.7	24	8	US-10-310-914A-317201	Sequence 317201,
C 124	23	1.7	23	8	US-10-310-914A-167370	Sequence 167370,	C 197	23	1.7	24	8	US-10-310-914A-339018	Sequence 339018,
C 125	23	1.7	23	8	US-10-310-914A-167688	Sequence 167688,	C 198	23	1.7	24	8	US-10-310-914A-341341	Sequence 341341,
C 126	23	1.7	23	8	US-10-310-914A-167689	Sequence 167689,	C 199	23	1.7	24	8	US-10-310-914A-341342	Sequence 341342,
C 127	23	1.7	23	8	US-10-310-914A-168050	Sequence 168050,	C 200	23	1.7	24	8	US-10-310-914A-341343	Sequence 341343,
C 128	23	1.7	23	8	US-10-310-914A-168051	Sequence 168051,	C 201	23	1.7	24	8	US-10-310-914A-341344	Sequence 341344,
C 129	23	1.7	23	8	US-10-310-914A-168052	Sequence 168052,	C 202	23	1.7	24	8	US-10-310-914A-368121	Sequence 368121,
C 130	23	1.7	23	8	US-10-310-914A-168053	Sequence 168053,	C 203	23	1.7	24	8	US-10-310-914A-412089	Sequence 412089,
C 131	23	1.7	23	8	US-10-310-914A-168054	Sequence 168054,	C 204	23	1.7	24	8	US-10-310-914A-412090	Sequence 412090,
C 132	23	1.7	23	8	US-10-310-914A-168055	Sequence 168055,	C 205	23	1.7	24	8	US-10-310-914A-412091	Sequence 412091,
C 133	23	1.7	23	8	US-10-310-914A-168056	Sequence 168056,	C 206	23	1.7	24	8	US-10-310-914A-412092	Sequence 412092,
C 134	23	1.7	23	8	US-10-310-914A-168057	Sequence 168057,	C 207	23	1.7	24	8	US-10-310-914A-430467	Sequence 430467,
C 135	23	1.7	23	8	US-10-310-914A-182888	Sequence 182888,	C 208	23	1.7	24	8	US-10-310-914A-494510	Sequence 494510,
C 136	23	1.7	23	8	US-10-310-914A-182892	Sequence 182892,	C 209	23	1.7	24	8	US-10-310-914A-494511	Sequence 494511,
C 137	23	1.7	23	8	US-10-310-914A-182893	Sequence 182893,	C 210	23	1.7	24	8	US-10-310-914A-632071	Sequence 632071,
C 138	23	1.7	23	8	US-10-310-914A-182894	Sequence 182894,	C 211	23	1.7	24	8	US-10-310-914A-641630	Sequence 641630,
C 139	23	1.7	23	8	US-10-310-914A-226060	Sequence 226060,	C 212	23	1.7	24	8	US-10-310-914A-691360	Sequence 691360,
C 140	23	1.7	23	8	US-10-310-914A-226061	Sequence 226061,	C 213	23	1.7	24	8	US-10-310-914A-816478	Sequence 816478,
C 141	23	1.7	23	8	US-10-310-914A-226062	Sequence 226062,	C 214	23	1.7	24	8	US-10-310-914A-844403	Sequence 844403,
C 142	23	1.7	23	8	US-10-310-914A-226063	Sequence 226063,	C 215	23	1.7	24	8	US-10-310-914A-845281	Sequence 845281,
C 143	23	1.7	23	8	US-10-310-914A-226064	Sequence 226064,	C 216	23	1.7	24	8	US-10-310-914A-938142	Sequence 938142,
C 144	23	1.7	23	8	US-10-310-914A-255935	Sequence 255935,	C 217	23	1.7	24	8	US-10-310-914A-981803	Sequence 981803,
C 145	23	1.7	23	8	US-10-310-914A-261088	Sequence 261088,	C 218	23	1.7	24	8	US-10-310-914A-981804	Sequence 981804,
C 146	23	1.7	23	8	US-10-310-914A-346663	Sequence 346663,	C 219	23	1.7	24	8	US-10-310-914A-981805	Sequence 981805,
C 147	23	1.7	23	8	US-10-310-914A-446664	Sequence 446664,	C 220	23	1.7	24	8	US-10-310-914A-130946	Sequence 130946,
C 148	23	1.7	23	8	US-10-310-914A-399955	Sequence 399955,	C 221	23	1.7	24	8	US-10-310-914A-1090775	Sequence 1090775,
C 149	23	1.7	23	8	US-10-310-914A-399984	Sequence 399984,	C 222	23	1.7	24	8	US-10-310-914A-1090775	Sequence 1090775,
C 150	23	1.7	23	8	US-10-310-914A-399995	Sequence 399995,	C 223	23	1.7	24	8	US-10-310-914A-130943	Sequence 130943,
C 151	23	1.7	23	8	US-10-310-914A-399999	Sequence 399999,	C 224	23	1.7	24	8	US-10-310-914A-130944	Sequence 130944,
C 152	23	1.7	23	8	US-10-310-914A-416111	Sequence 416111,	C 225	23	1.7	24	8	US-10-310-914A-130945	Sequence 130945,
C 153	23	1.7	23	8	US-10-310-914A-430461	Sequence 430461,	C 226	23	1.7	24	8	US-10-310-914A-130946	Sequence 130946,
C 154	23	1.7	23	8	US-10-310-914A-432629	Sequence 432629,	C 227	23	1.7	24	8	US-10-310-914A-130947	Sequence 130947,
C 155	23	1.7	23	8	US-10-310-914A-463744	Sequence 463744,	C 228	23	1.7	24	8	US-10-310-914A-130948	Sequence 130948,
C 156	23	1.7	23	8	US-10-310-914A-463745	Sequence 463745,	C 229	23	1.7	24	8	US-10-310-914A-130949	Sequence 130949,
C 157	23	1.7	23	8	US-10-310-914A-536246	Sequence 536246,	C 230	23	1.7	25	8	US-10-310-914A-51711	Sequence 51711, A
C 158	23	1.7	23	8	US-10-310-914A-536250	Sequence 536250,	C 231	23	1.7	25	8	US-10-310-914A-948350	Sequence 948350,
C 159	23	1.7	23	8	US-10-310-914A-545337	Sequence 545337,	C 232	23	1.7	25	8	US-10-310-914A-169350	Sequence 169350,
C 160	23	1.7	23	8	US-10-310-914A-545438	Sequence 545438,	C 233	23	1.7	25	8	US-10-310-914A-280847	Sequence 280847,
C 161	23	1.7	23	8	US-10-310-914A-576634	Sequence 576634,	C 234	23	1.7	25	8	US-10-310-914A-412093	Sequence 412093,
C 162	23	1.7	23	8	US-10-310-914A-807660	Sequence 807660,	C 235	23	1.7	25	8	US-10-310-914A-633080	Sequence 633080,
C 163	23	1.7	23	8	US-10-310-914A-838215	Sequence 838215,	C 236	23	1.7	25	8	US-10-310-914A-641631	Sequence 641631,
C 164	23	1.7	23	8	US-10-310-914A-875272	Sequence 875272,	C 237	23	1.7	25	8	US-10-310-914A-691353	Sequence 691353,
C 165	23	1.7	23	8	US-10-310-914A-983802	Sequence 983802,	C 238	23	1.7	25	8	US-10-310-914A-816473	Sequence 816473,
C 166	23	1.7	26	8	US-10-310-914A-1008724	Sequence 1008724,	C 239	23	1.7	25	8	US-10-310-914A-816473	Sequence 816473,

C 240	23	1.7	25	8	US-10-310-914A-844404	Sequence 844404, A	C 313	23	1.7	2690	9	US-11-072-512-608	Sequence 608, App
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C 242	23	1.7	25	8	US-10-310-914A-938143	Sequence 938143, A	C 315	23	1.7	2804	12	US-11-241-347-2	Sequence 2, App1
C 243	23	1.7	25	8	US-10-310-914A-969285	Sequence 969285, A	C 316	23	1.7	3050	12	US-11-136-527-3575	Sequence 3575, App
C 244	23	1.7	26	8	US-10-310-914A-51710	Sequence 51710, A	C 317	23	1.7	3073	12	US-11-113-424-11	Sequence 11, App1
C 245	23	1.7	26	8	US-10-310-914A-255939	Sequence 255939, A	C 318	23	1.7	3108	8	US-10-514-863-1	Sequence 1, App1
C 246	23	1.7	26	8	US-10-310-914A-983806	Sequence 983806, A	C 319	23	1.7	3147	8	US-10-477-507A-1	Sequence 1, App1
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C 259	23	1.7	344	6	US-09-925-065A-508378	Sequence 508378, A	C 332	23	1.7	5011	7	US-10-826-585-15	Sequence 35, App1
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C 262	23	1.7	399	12	US-11-136-527-1868	Sequence 1868, App	C 335	23	1.7	5213	12	US-11-136-527-3578	Sequence 3578, App
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C 266	23	1.7	481	6	US-09-925-065A-281107	Sequence 281107, A	C 339	23	1.7	11564	12	US-11-000-688-860	Sequence 860, App
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C 270	23	1.7	542	6	US-09-925-065A-161188	Sequence 161188, A	C 343	23	1.7	13054	12	US-11-121-086-56	Sequence 56, App1
C 271	23	1.7	542	6	US-09-925-065A-161189	Sequence 161189, A	C 344	23	1.7	157224	12	US-11-121-086-51	Sequence 51, App1
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C 273	23	1.7	580	6	US-09-925-065A-309841	Sequence 309841, A	C 346	23	1.7	16816	12	US-11-112-908-59	Sequence 59, App1
C 274	23	1.7	582	6	US-09-925-065A-309842	Sequence 309842, A	C 347	23	1.7	170189	12	US-11-112-908-58	Sequence 58, App1
C 275	23	1.7	582	6	US-09-925-065A-309843	Sequence 309843, A	C 348	23	1.7	170189	12	US-11-112-908-58	Sequence 58, App1
C 276	23	1.7	582	6	US-09-925-065A-309844	Sequence 309844, A	C 349	23	1.7	170189	12	US-11-112-908-58	Sequence 58, App1
C 277	23	1.7	585	6	US-09-925-065A-908301	Sequence 908301, A	C 350	23	1.7	172543	12	US-11-121-086-6	Sequence 6, App1
C 278	23	1.7	602	6	US-09-925-065A-507497	Sequence 507497, A	C 351	23	1.7	172543	12	US-11-121-086-6	Sequence 6, App1
C 279	23	1.7	614	6	US-09-925-065A-507494	Sequence 507494, A							
C 280	23	1.7	614	6	US-09-925-065A-507496	Sequence 507496, A							
C 281	23	1.7	614	6	US-09-925-065A-75381	Sequence 75381, A							
C 282	23	1.7	644	6	US-09-925-065A-74775	Sequence 74775, A							
C 283	23	1.7	650	9	US-11-031-206-185	Sequence 185, App							
C 284	23	1.7	687	6	US-09-925-065A-507495	Sequence 507495, A							
C 285	23	1.7	688	6	US-09-925-065A-6249	Sequence 6249, App							
C 286	23	1.7	688	6	US-09-925-065A-6250	Sequence 6250, App							
C 287	23	1.7	688	6	US-09-925-065A-6251	Sequence 6251, App							
C 288	23	1.7	688	6	US-09-925-065A-6252	Sequence 6252, App							
C 289	23	1.7	717	7	US-10-714-887-123	Sequence 123, App							
C 290	23	1.7	837	7	US-10-714-887-335	Sequence 335, App							
C 291	23	1.7	843	12	US-11-071-062-4	Sequence 4, App1							
C 292	23	1.7	852	8	US-10-750-185-63402	Sequence 63402, A							
C 293	23	1.7	852	8	US-10-750-623-63402	Sequence 63402, A							
C 294	23	1.7	882	12	US-11-071-062-6	Sequence 6, App1							
C 295	23	1.7	909	8	US-10-750-185-41862	Sequence 41862, A							
C 296	23	1.7	909	8	US-10-750-623-41862	Sequence 41862, A							
C 297	23	1.7	992	12	US-11-136-527-1674	Sequence 1674, App							
C 298	23	1.7	992	12	US-11-136-527-5770	Sequence 5770, App							
C 299	23	1.7	1088	6	US-09-925-065A-69151	Sequence 69151, A							
C 300	23	1.7	1107	7	US-10-888-6138-7	Sequence 7, App1							
C 301	23	1.7	1291	12	US-11-071-062-10	Sequence 10, App1							
C 302	23	1.7	1393	12	US-11-051-267-24	Sequence 24, App1							
C 303	23	1.7	1400	12	US-11-136-527-7671	Sequence 7671, App							
C 304	23	1.7	1437	12	US-11-121-438-7	Sequence 7, App1							
C 305	23	1.7	1478	8	US-10-775-169-262	Sequence 262, App							
C 306	23	1.7	1685	12	US-11-057-012-63	Sequence 63, App1							
C 307	23	1.7	1944	12	US-11-136-527-3818	Sequence 3818, App							
C 308	23	1.7	2175	12	US-11-136-527-2262	Sequence 2262, App							
C 309	23	1.7	2187	9	US-11-245-147-141	Sequence 141, App							
C 310	23	1.7	2400	9	US-11-072-512-228	Sequence 228, App							
C 311	23	1.7	2500	9	US-11-245-147-210	Sequence 210, App							
C 312	23	1.7	2690	9	US-11-072-512-608	Sequence 608, App							

RESULT 1  
 US-11-186-284-208  
 ; Sequence 208, Application US/11186284  
 ; Publication No. US20050266493A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Berger, Allison  
 ; APPLICANT: Guillemette, Tracy L.  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Schlegel, Robert  
 ; APPLICANT: Monahan, John E.  
 ; APPLICANT: Thibodeau, Stephen N.  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; FILE REFERENCE: MPW01-029P2RNM  
 ; CURRENT APPLICATION NUMBER: US/11/186,284  
 ; CURRENT FILING DATE: 2005-07-21  
 ; PRIOR APPLICATION NUMBER: US/10/301,822  
 ; PRIOR FILING DATE: 2002-11-21  
 ; PRIOR APPLICATION NUMBER: US 60/339,971  
 ; PRIOR FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/361,978  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 60/381,988  
 ; PRIOR FILING DATE: 2002-05-20  
 ; NUMBER OF SEQ ID NOS: 228  
 ; SOFTWARE: FastSeq for Windows Version 4.0





```
;; APPLICANT: Shiler, Kyuzat
;; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;; FILE OF INVENTION: uses thereof
;; FILE REFERENCE: 06087.0200.CPUS01
;; CURRENT APPLICATION NUMBER: US/10/310,914A
;; NUMBER OF SEQ ID NOS: 1388402
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 1106
;; LENGTH: 94
;; TYPE: RNA
;; ORGANISM: Human
US-10-310-914A-1106

Query Match
Best Local Similarity 100.0%; Pred. No. 9.3e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1028 TGCCCCCAGCAGTAATCTGGGCGATCGCCGCAAGTGTCTACGCGAGGGGGGGCGCATG 1087
DB 79 TGCCCCCAGCAGTAATCTGGGCGATCGCCGCAAGTGTCTACGCGAGGGGGGGCGCATG 20
QY 1088 GAGGGGGCGCGCCGACCT 1106
DB 19 GAGGGGGCGCGCCGACCT 1

RESULT 5
US-10-310-914A-1107/c
; Sequence 1107, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1107
; LENGTH: 97
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1107

Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 TGGAGCAAGAGAGAGATTAAGAGAGACCCCTCTAGAGTCCCGAGGGGGGGCGG 1294
DB 72 TGGAGCAAGAGAGAGATTAAGAGAGACCCCTCTAGAGTCCCGAGGGGGGGCGG 13
QY 1295 GCTGGGGCTGCG 1306
DB 12 GCTGGGGCTGCG 1

RESULT 6
US-10-310-914A-7162/c
; Sequence 7162, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; NUMBER OF SEQ ID NOS: 1388402
```

```
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 7162
;; LENGTH: 63
;; TYPE: RNA
;; ORGANISM: Human
US-10-310-914A-7162

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1130 CCGGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGCGCCCTCTGCTG 1180
DB 63 CCGGGGTCTCTCTTCAGACACAGCAGAGAGAGTGGCGCCCTCTGCTG 13

RESULT 7
US-11-072-512-700/c
; Sequence 700, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; NUMBER OF SEQ ID NOS: 2005-03-07
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 700
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-700

Query Match
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGAGAGAGAGCGCGCGCGCGCGCGG 75
DB 1225 GAGGAGAGAGAGCGCGCGCGCGCGCGG 1195

RESULT 8
US-10-310-914A-399937/c
; Sequence 399937, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
```

FILE REFERENCE: 06087.0200.CPUS01  
CURRENT APPLICATION NUMBER: US/10/310.914A  
CURRENT FILING DATE: 2002-12-06  
NUMBER OF SEQ ID NOS: 1388402  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 399937  
LENGTH: 30  
TYPE: RNA  
ORGANISM: Human  
US-10-310-914A-399937

Query Match 2.2%; Score 29; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1284 AGGGGGCGGGGCTGGGGCTGCGTAGGTG 1312  
DB 29 AGGGGGCGGGGCTGGGGCTGCGTAGGTG 1

RESULT 9  
US-11-112-944-14  
Sequence 14, Application US/11112944  
Publication No. US20050244872A1  
GENERAL INFORMATION:  
APPLICANT: Harris, Cole

TITLE OF INVENTION: Breast Cancer Gene Expression Biomarkers  
FILE REFERENCE: 05-325-US  
CURRENT APPLICATION NUMBER: US/11/112.944  
CURRENT FILING DATE: 2005-04-22  
PRIOR APPLICATION NUMBER: US 60/564,757  
PRIOR FILING DATE: 2004-04-23  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 14  
LENGTH: 1546  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-112-944-14

Query Match 2.2%; Score 29; DB 10; Length 1546;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84  
DB 439 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 467

RESULT 10  
US-11-136-527-144/C  
Sequence 144, Application US/11136527  
Publication No. US20050287570A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth

TITLE OF INVENTION: Mounts, William M  
FILE REFERENCE: 031896-041000 (AM101086)  
CURRENT APPLICATION NUMBER: US/11/136.527  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US 60/574,294  
PRIOR FILING DATE: 2005-05-26  
NUMBER OF SEQ ID NOS: 362830  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 144  
LENGTH: 2947  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-11-136-527-144

Query Match 2.2%; Score 29; DB 12; Length 2947;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 81  
DB 85 GGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57

RESULT 11  
US-10-770-726-28/C  
Sequence 28, Application US/10770726  
Publication No. US20050266409A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
FILE REFERENCE: AM101079 (031896-010000)  
CURRENT APPLICATION NUMBER: US/10/770.726  
CURRENT FILING DATE: 2004-02-04  
NUMBER OF SEQ ID NOS: 48640  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 28  
LENGTH: 3131  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-770-726-28

Query Match 2.2%; Score 29; DB 8; Length 3131;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 TGAGGAGGAGGAGGAGGCGCGCGCGCGCGCGG 72  
DB 227 TGAGGAGGAGGAGGAGGCGCGCGCGCGCGCGG 199

RESULT 12  
US-11-121-086-14  
Sequence 14, Application US/11121086  
Publication No. US20050266459A1  
GENERAL INFORMATION:  
APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION: NIELSEN, KIRSTEN V.  
FILE REFERENCE: 09138.6000-00000  
CURRENT APPLICATION NUMBER: US/11/121.086  
CURRENT FILING DATE: 2005-05-04  
PRIOR APPLICATION NUMBER: 60/567,570  
PRIOR FILING DATE: 2004-05-04  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 14  
LENGTH: 167891  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-121-086-14

Query Match 2.2%; Score 29; DB 12; Length 167891;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84  
DB 100185 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 100213

RESULT 13  
US-10-310-914A-100326  
Sequence 100326, Application US/10310914A  
Publication No. US20060003322A1  
GENERAL INFORMATION:  
APPLICANT: Benitich, Isaac  
APPLICANT: Shlter, Kwuzat



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4204
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4204
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      142 GAGGAGCGCGCGCGCGCGCGCGCGCGG 115
```

```
RESULT 18
US-11-124-367A-4257/c
; Sequence 4257, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4257
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4257
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      138 GAGGAGCGCGCGCGCGCGCGCGCGCGG 111
```

```
RESULT 19
US-11-124-367A-4261/c
; Sequence 4261, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4261
; LENGTH: 201
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4261
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      96 GAGGAGCGCGCGCGCGCGCGCGCGCGG 69
```

```
RESULT 20
US-11-124-367A-4262/c
; Sequence 4262, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4262
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4262
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      40 GAGGAGCGCGCGCGCGCGCGCGCGCGG 13
```

```
RESULT 21
US-11-124-367A-4274/c
; Sequence 4274, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4274
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4274
```

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGGCGGCGGCGGCGGCGGCGG 78  
DB 142 GAGGAGGCGGCGGCGGCGGCGGCGG 115

RESULT 22  
US-11-124-367A-4325/C  
; Sequence 4325, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4325  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-4325

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGGCGGCGGCGGCGGCGGCGG 78  
DB 138 GAGGAGGCGGCGGCGGCGGCGGCGG 111

RESULT 23  
US-11-124-367A-4329/C  
; Sequence 4329, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4329  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-4329

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGGCGGCGGCGGCGGCGGCGG 78  
DB 96 GAGGAGGCGGCGGCGGCGGCGGCGG 69

RESULT 24  
US-11-124-367A-4330/C  
; Sequence 4330, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4330  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-4330

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGGCGGCGGCGGCGGCGGCGG 78  
DB 40 GAGGAGGCGGCGGCGGCGGCGGCGG 13

RESULT 25  
US-11-124-367A-4342/C  
; Sequence 4342, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4342  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-4342

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGGCGGCGGCGGCGGCGGCGG 78

Db 142 GAGGAGCGCGCGCGCGCGCGCGG 115

```
RESULT 26
US-11-124-367A-4392/c
; Sequence 4392, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C0001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4392
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4392
```

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78  
Db 138 GAGGAGCGCGCGCGCGCGCGCGG 111

```
RESULT 27
US-11-124-367A-4396/c
; Sequence 4396, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C0001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4396
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4396
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Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78  
Db 96 GAGGAGCGCGCGCGCGCGCGCGG 69

```
RESULT 28
US-11-124-367A-4397/c
; Sequence 4397, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C0001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4397
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4397
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Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78  
Db 40 GAGGAGCGCGCGCGCGCGCGCGG 13

```
RESULT 29
US-11-124-367A-4409/c
; Sequence 4409, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C0001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4409
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4409
```

Query Match 2.1%; Score 28; DB 12; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78  
Db 142 GAGGAGCGCGCGCGCGCGCGCGG 115

RESULT 30  
US-11-124-367A-23494/c

Publication No. US20060010516A1

GENERAL INFORMATION:

APPLICANT: FORSTER, RICHARD L.

APPLICANT: CONNETT, MARIE B.

APPLICANT: EMERSON, SARAH JANE



RESULT 38  
US-11-124-367A-204/C  
: Sequence 204, Application US/1124367A  
: Publication No. US20060024700A1  
: GENERAL INFORMATION:  
: APPLICANT: Michele Cargill  
: APPLICANT: Hongjin Huang  
: TITLE OF INVENTION: Genetic Polymorphisms Associated with  
: TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
: FILE REFERENCE: CL001519.0KD  
: CURRENT APPLICATION NUMBER: US/11/124.367A  
: PRIOR APPLICATION NUMBER: US 60/568,846  
: PRIOR FILING DATE: 2004-05-07  
: PRIOR APPLICATION NUMBER: US 60/582,609  
: PRIOR FILING DATE: 2004-06-25  
: PRIOR APPLICATION NUMBER: US 60/599,554  
: PRIOR FILING DATE: 2004-08-09



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; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087,0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20511
; LENGTH: 110
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-20511

Query Match          2.0%; Score 27; DB 8; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 AGAGAGCGCGCGCGCGCGCGCGCGCG 75
Db 79 AGGAGGAGCGCGCGCGCGCGCGCGCG 105

RESULT 44
US-09-925-065A-373740/c
; Sequence 373740, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373740
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-373740

Query Match          2.0%; Score 27; DB 6; Length 552;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GCGCGCGCGCGCGCGCGCGCGCGAGGC 82
Db 305 GCGCGCGCGCGCGCGCGCGCGCGAGGC 279

RESULT 45
US-09-925-065A-540849
; Sequence 540849, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540849
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-540849

Query Match          2.0%; Score 27; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 AGAGGCGCGCGCGCGCGCGCGCGCG 78
Db 412 AGGAGGCGCGCGCGCGCGCGCGCG 438

RESULT 46
US-09-925-065A-540850
; Sequence 540850, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540850
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-540850

Query Match          2.0%; Score 27; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 AGAGGCGCGCGCGCGCGCGCGCGCG 78
Db 412 AGGAGGCGCGCGCGCGCGCGCGCG 438

RESULT 47
US-09-925-065A-499554/c
; Sequence 499554, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

```

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 499554
; LENGTH: 665
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-499554

Query Match
Best Local Similarity 2.0%; Score 26; DB 6; Length 665;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

56 GGCGCGCGCGCGCGCGCGCGGAG 81
189 GGCGCGCGCGCGCGCGCGCGGAG 164

RESULT 48
US-11-136-527-2759
; Sequence 2759, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2759
; LENGTH: 1598
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2759

Query Match
Best Local Similarity 2.0%; Score 26; DB 12; Length 1598;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

50 GGAGGAGGCGCGCGCGCGCGCGG 75
499 GGAGGAGGCGCGCGCGCGCGCGG 524

RESULT 49
US-11-136-527-2522
; Sequence 2522, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
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; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2522
; LENGTH: 2074
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2522

Query Match
Best Local Similarity 2.0%; Score 26; DB 12; Length 2074;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GGAGCGCGCGCGCGCGCGCGGCGG 78
262 GGAGCGCGCGCGCGCGCGCGGCGG 287

RESULT 50
US-10-750-185-34757
; Sequence 34757, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34757
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Bovine
; US-10-750-185-34757

Query Match
Best Local Similarity 2.0%; Score 26; DB 8; Length 2127;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

53 GGAGCGCGCGCGCGCGCGCGGCGG 78
1117 GGAGCGCGCGCGCGCGCGCGGCGG 1142

Search completed: February 28, 2006, 11:27:00
Job time : 485 secs
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 08:31:33 ; Search time 7076.01 Seconds  
(without alignments)  
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Title: US-09-934-249-1

Perfect score: 1321  
Sequence: 1 cgaccgcgctcgcgagcga.....ctgcgtagctgcaaaagcag 1321

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5683141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

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1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_ph:\*  
9: gb\_ph:\*  
10: gb\_ph:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	AX392417 Sequence
2	1302	98.6	4930	6	CS130796 Sequence
3	1229	93.0	4839	6	CQ812357 Sequence
4	1229	93.0	4839	6	CQ896247 Sequence
5	1229	93.0	4839	6	CQ976475 Sequence
6	1229	93.0	4839	6	CQ981430 Sequence
7	1229	93.0	4839	6	AF305616 Sequence
8	1227.4	92.9	1383	6	AX775889 Sequence
9	909	68.8	4519	6	CQ894692 Sequence
10	887.4	67.2	1061	8	BC015918 Homo sapi
11	861	65.2	861	6	AX392419 Sequence
12	803.2	60.8	969	6	BD272494 Secretd
13	802.2	60.7	1141	8	AF224278 Homo sapi
14	802.2	60.7	4538	6	CS130841 Sequence
15	801.8	60.7	1913	6	BD272544 Secretd
16	801.6	60.7	969	6	BD272514 Secretd
17	801.6	60.7	969	6	BD272515 Secretd
18	801.6	60.7	969	6	BD272516 Secretd

19	801.6	60.7	1140	6	AR336830 Sequence
20	800.6	60.6	1085	6	AX775887 Sequence
21	800	60.6	1818	8	AY128643 Homo sapi
22	800	60.6	4531	8	CS130842 Sequence
23	797.4	60.4	1060	8	BC080635 Homo sapi
24	755.8	57.2	759	6	AR336831 Sequence
25	755.4	57.2	756	6	BD272545 Secretd
26	751.2	56.9	756	6	BD272495 Secretd
27	750.4	56.8	753	6	BD272513 Secretd
28	630	47.7	1379	9	BC036995 Mus muscu
29	618.6	46.8	1079	9	BC023092 Mus muscu
30	616.4	46.7	878	6	AX392428 Sequence
31	614.6	46.5	878	9	BC092094 Mus muscu
32	600	45.4	600	6	C0728942 Sequence
33	594.4	45.0	61505	8	AF305426 Homo sapi
34	594.4	45.0	130435	8	HS17807 Human DNA
35	589.2	44.6	1583	6	AX593655 Sequence
36	588	44.5	895	6	BC069890 Mus muscu
37	565.6	42.8	1265	5	AJ720618 Gallus ga
38	522.8	39.6	150224	8	HS105917 Human DNA
39	493.6	37.4	693	6	AX392430 Sequence
40	468.6	35.5	158243	14	CR956387 Sus scro
41	468.6	35.5	183457	14	CR956387 Sus scro
42	466.2	35.3	1713	6	BD272504 Secretd
43	464.6	35.2	1713	6	BD272517 Secretd
44	464.6	35.2	1713	6	BD272518 Secretd
45	464.6	35.2	1713	6	BD272519 Secretd

#### ALIGNMENTS

RESULT 1	AX392417	1321 bp	DNA	linear	PAT 23-MAR-2002
LOCUS	AX392417	Sequence 1 from Patent WO0216416.			
DEFINITION	AX392417				
ACCESSION	AX392417.1	GI:19700732			
VERSION	AX392417.1	GI:19700732			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Lee,R.T., Landschulz,K.T., Kennedy,S.P., Thompson,J.F. and Turi,T.G.				
AUTHORS					
TITLE	Diagnosis and treatment of cardiovascular conditions				
JOURNAL	Patent: WO 0216416-A.1 28-FEB-2002;				
FEATURES	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)				
source	Location/Qualifiers				
CDS	1..1321				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
	413..1276				
	/note="unassigned protein product"				
	/codon_start=1				
	/protein_id="CAD29005.1"				
	/db_xref="GI:19700732"				
	/translation="MHRLMGVNSRAAAGQPNVSCNCRKSLFQSMETLEFVQI IIVVMMVAVITCLSHYKLSARSTISHSGQRREDLSSGCIWPSRSTVSGN GIPEQVYAPRPFDRLAVPFAQERFHPOTYPIVSHIDLPFTISLDSGEPP YQGETTQLRDEQLELRNSVAPRPFITFSDLDMSATLGGCPSSSGSATC YGGGRMGPEPTSEVIGHYFGSSFFHQSSGPPSLGLETRLHTHTIAPLESATWS KEKQKXKHPL"				
ORIGIN					
Query Match	100.0%; Score 1321; DB 6; Length 1321;				
Best Local Similarity	100.0%; Pred. No. 5.3e-142;				
Matches 1321; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 CGACCGCGCTCGAGGAAACCGGATCTCTTGACTTAATGAGGAGGAGGCGG 60				

```

Db      1 CGACCGCGGTCTCGAGAGGAAACCGGANTCTCTTGATCTTGAATGAGAGGAGAGGCGG 60
Qy      61 CGCGCGCGCGCGCGCGCGCGCGCTCGCTGCGGAAAGCTAGCGGACAGAGGCTAGACCCC 120
Db      61 CGCGCGCGCGCGCGCGCGCGCGCTCGCTGCGGAAAGCTAGCGGACAGAGGCTAGACCCC 120
Qy      121 GCGCGGAGCGCGCGCGCGCGCGCGCTGCGGAGCCATTTTTCGCGAGCGCACCGCGCGGCACTGCGG 180
Db      121 GCGCGGAGCGCGCGCGCGCGCGCGCTGCGGAGCCATTTTTCGCGAGCGCACCGCGCGGCACTGCGG 180
Qy      181 ACGCCCGCGGCGCTGCCGAGGAGGAGCGCGGCGGCGCGAGCGAGCGCGGCTCCGCGCAC 240
Db      181 ACGCCCGCGGCGCTGCCGAGGAGGAGCGCGGCGGCGCGAGCGAGCGCGGCTCCGCGCAC 240
Qy      241 TGAAGCGCGCGCGCGCGCGGAACTTGGCGGCGAGCCGAGCGCGGCGCGCGCGCG 300
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Qy      361 CCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATGCA 420
Db      361 CCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATGCA 420
Qy      421 CTGATGCGGCGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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Qy      481 GTGCAACTGCAAAAGCTCTTGTTCAGAGCATGAGATCAAGAGCTGAGATTGTTCAC 540
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Qy      541 GATCATCATCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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Qy      601 CCACTAACAAGCTGTCTGCAAGCGGTCTTATCATCAGCGGACAGCGGCGGAGAGAGA 660
Db      601 CCACTAACAAGCTGTCTGCAAGCGGTCTTATCATCAGCGGACAGCGGCGGAGAGAGA 660
Qy      661 AGATGCCCTGTCTCTGAGAAAGATGCTGTGCGCTCGGAGAGGACAGGTCTAGAGGAA 720
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Db      721 AATCCAGAGCGCGAGGTCTAGCGCGCGCTCGGCGCGCACCGAGCGCGCTGCGCGCC 780
Qy      781 CTTCGCCAGCGGAGCGCTTCCACCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCC 840
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Qy      841 GATGCACTGTGCAACCACTCTGTGCTGCAAGCGGAGAGAGCGCGCGCGCGCGCGCG 900
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Db      1021 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
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Qy      1201 CACACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
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Qy      1261 AGGACACCTCTCTTGAAGGTCCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
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Db      1321 G 1321

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LOCUS      CS130796      4930 bp      DNA      linear      PAT 02-AUG-2005
DEFINITION      Sequence 82 from Patent WO2005064009.
ACCESSION      CS130796
VERSION      CS130796.1 GI:71792866
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1. Ornoff, T. F.
  Classification of cancer
  Patent: WO 2005064009-A 82 14-JUL-2005;
  Aros Applied Biotechnology APS (DX)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5; Se-140; Indels 0; Gaps 0;
Matches 1302; Conservative 0; Mismatches 0;
Qy      20 AACCCGATCTCTTGAAGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 79
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Qy      140 CTGCGACCCATTTTCCGAGAGCGCAACCGCGGCGACTGCGAGCGCGCGCGCGCGCG 199
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Qy      200 GGGAGGCGGGGAGGAGCGAGAGAGCGGCTCCCGCGCACTAGAGCGCGCGCGCGCG 259
Db      181 GGGAGGCGGGGAGGAGCGAGAGAGCGGCTCCCGCGCACTAGAGCGCGCGCGCGCG 240
Qy      260 GGAACCTTGGCGGAGCGCGAGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 319
Db      241 GGAACCTTGGCGGAGCGCGAGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy      320 CTGATGCGGGGCGCGCGAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 379
Db      301 CTGATGCGGGGCGCGCGAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy      380 CCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 439

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QY 993 GTGACCTGATGATAGTGCACAGGCTGAGCGGCCCCCTGCCCCCAAGATTAATCTGGGCA 1052  
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RESULT 4  
LOCUS CO896247 4839 bp DNA linear PAT 05-NOV-2004  
DEFINITION Sequence 71 from Patent WO2004076614.  
ACCESSION CO896247  
VERSION CO896247.1 GI:55468096  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
AUTHORS Hitzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A.,  
Beckmann, G., Bruemendorf, T., Kinneemann, H., Roeper, S., Hermann, K.,  
Xinzhong, J., Pilarsky, C. and Staud, B.  
TITLE Human nucleic acid sequences obtained from prostatic carcinomas  
JOURNAL Patient: WO 2004076614-A 71 10-SEP-2004;  
Hitzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);  
Specht, Thomas (DE); Schmitt, Armin (DE)  
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Query Match 93.0%; Score 1229; DB 6; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 1,2e-111;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 153 TTCCGAGCGCACCCCGCGGCGCACTGCGACGCGCCCGGCGGCTGCGAGAGGAGCGGG 212  
Db 61 TTCCGAGCGCACCCCGCGGCGCACTGCGACGCGCCCGGCGGCTGCGAGAGGAGCGGG 120

QY 213 GGGCGAGCGGAGCGCGGTCCCGGCACTGAGCCCGCGGCGCGCCCGGAGAACTTGGCGG 272  
Db 121 GGGCGAGCGGAGCGCGGTCCCGGCACTGAGCCCGCGGCGCGCCCGGAGAACTTGGCGG 180  
QY 273 GACCCGAGCCCGGCGAGCCCGGCGCGCTTCCCGCGCGCGCTTCTGATGCGGGGC 332  
Db 181 GACCCGAGCCCGGCGAGCCCGGCGCGCTTCCCGCGCGCGCTTCTGATGCGGGGC 240  
QY 333 CCCAGCTCCCGGCGCGCGCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392  
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QY 393 GCGCGCGCGCGCGCGCTCCATGCAACCGCTTGAATGGGGGTCAACAGACCGCGCGCG 452  
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RESULT 5  
LOCUS CQ976475 4839 bp DNA linear PAT 19-JAN-2005  
DEFINITION Sequence 166 from Patent WO2004113571.  
ACCESSION CQ976475  
VERSION CQ976475.1 GI:57975803  
KEYWORDS

SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Homnidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Einstein, R., McGowan, K.M. and Pando, M.P.  
JOURNAL Prostate specific genes and the use thereof as targets for prostate  
cancer therapy and diagnosis  
Patent: WO 2004113571-A 166 29-DEC-2004;  
Exonhit Therapeutics S.A. (FR)  
FEATURES  
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QY 213 GGGCGGAGGAGCG 272  
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QY 273 GACCGGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 332  
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Db 481 TGGTGTGTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
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RESULT 6  
LOCUS CQ981430 4839 bp DNA linear PAT 25-JAN-2005  
DEFINITION Sequence 285 from Patent EP1498424.  
ACCESSION CQ981430  
VERSION CQ981430.1 GI:58190720  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS 1  
TITLE Rosenthal, A., Hermann, K., Heiden, E., Pilarsky, C., Bruemendorf, T.,  
Staub, E., Roepcke, S., Mennertich, D., Kinneemann, H. and Li, X.  
JOURNAL Human nucleic acid sequences from lung tumours  
Patent: EP 1498424-A 285 19-JAN-2005;  
Hinzmann, Bernd (DB); Hermann, Klaus (DB); Heiden, Esmeralda (DB);  
Rosenthal, Andre (DB)  
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SOURCE Location/Qualifiers  
1. 4839  
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ORIGIN  
Query Match 93.0%; Score 1229; DB 6; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 1.2e-131;



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RESULT 8  
AX75889 1383 bp mRNA linear PAT 14-JUN-2003  
LOCUS Sequence 159 from Patent WO03048202.  
DEFINITION AX75889  
ACCESSION AX75889  
VERSION AX75889.1 GI:32693607  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
1 Matsuda, A. and Muramatsu, S.  
NF-kB activating gene  
TITLE Patent: WO 03048202-A 159 12-JUN-2003;  
JOURNAL Asehi Kasei Kabushiki Kaisha (JP)  
FEATURES  
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ORIGIN  
Query Match 92.9%; Score 1227.4; DB 6; Length 1383;  
Best Local Similarity 99.9%; Pred. No. 2.6e-131;  
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Dd	61 ACGCTCTTTGTTCCAGAGCATGAGATCAAGAGTGAGTGTGTTTCAGATCATCATCAT 120
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DEFINITION Sequence 3 from Patent WO0216416.  
ACCESSION AX392419  
VERSION AX392419.1 GI:19700734  
KEYWORDS  
ORGANISM Homo sapiens (human)  
SOURCE Homo sapiens  
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Homnidae; Homo.  
REFERENCE 1  
Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and  
Turli, T.G.  
TITLE Diagnosis and treatment of cardiovascular conditions  
JOURNAL Patent: WO 0216416-A 3 28-FEB-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)  
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ACCESSION BD272494  
VERSION BD272494.1 GI:33082262  
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ORGANISM Homo sapiens  
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Homnidae; Homo.  
REFERENCE 1 (bases 1 to 969)



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Db	197	ACGGTCTTTCATCAGCCCGGCAACGCGAGGGGCGAGAGAGATGCTGTCTTCAGA	256
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VERSION	CS130841.1	GI:71792911			
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REFERENCE	1				
AUTHORS	Oernicoff, T.F.				
TITLE	Classification of cancer				
JOURNAL	Patent: WO 2005064009-A 127 14-JUN-2005;				
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Best Local Similarity 98.4%   Pred. No. 6.8e+83;
Matches 810, Conservative 0, Mismatches 13, Indels 0, Gaps 0

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Query Match	60.7%	Score 802.2	DB 6	Length 4538
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DEFINITION	Secreted proteins and nucleic acids encoding them.			PAT 17-JUL-200
ACCESSION	BD272544			
VERSION	BD272544.1			GI:33082312

KEYWORDS JP 2002539773-A/53.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 Homiidae; Homo.  
 1 (bases 1 to 1913)  
 AUTHORS Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.  
 TITLE Secreted proteins and nucleic acids encoding them  
 JOURNAL Patent: JP 2002539773-A 53 26-NOV-2002;  
 MILENNIUM PHARMACEUTICALS INC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002539773-A/53  
 PD 26-NOV-2002  
 PF 01-MAR-2000 JP 2000602247  
 PR 01-MAR-1999 US 60/122458  
 PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C  
 PI FRASER  
 PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC  
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GenCore version 5.1.7  
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5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	ABK12137 Human cDN
2	1302	98.6	4930	14	ABE22787 Human col
3	1301	98.5	4911	13	ACN40804 Tumour-as
4	1229	93.0	4839	8	ACC49552 Tumour-as
5	1229	93.0	4839	11	ADP65809 Human STA
6	1229	93.0	4839	11	ADP65729 Human tra
7	1229	93.0	4839	12	ADM67045 Human hom
8	1229	93.0	4839	13	ADR65875 Human pro
9	1229	93.0	4839	13	ADR66778 Human pro
10	1229	93.0	4839	13	ADU06063 Novel bro
11	1229	93.0	4839	14	ADM43368 Prostate
12	1227.4	92.9	1383	10	ADC37326 Nuclear f
13	909	68.8	4519	13	ADP97454 Pancreat
14	864	65.4	864	11	ADN38809 Cancer/an
15	803.2	60.7	1140	6	AA75151 cDNA enco
16	802.2	60.7	1141	10	ABK92120 Prostate
17	802.2	60.7	1850	8	ADP75568 Prostate
18	802.2	60.7	1850	8	ACC49536 Tumour-as
19	802.2	60.7	4527	11	ADL83313 Human and

20	802.2	60.7	4527	14	ADV85880 Human ARP
21	802.2	60.7	4538	14	ABE22832 Human col
22	801.6	60.7	969	3	AA75164 cDNA clon
23	801.6	60.7	969	3	AA75163 cDNA clon
24	801.6	60.7	969	3	AA75165 cDNA clon
25	801.6	60.7	1140	10	AD60105 Human and
26	801.6	60.7	1140	10	ADH62276 Human PME
27	801.6	60.7	1140	12	AD039826 Human PME
28	800.6	60.6	1061	3	AAA47429 Sequence
29	800.6	60.6	1085	10	ADC37324 Nuclear f
30	800.6	60.6	1334	8	ABZ36103 Human sec
31	800	59.8	4531	14	ABE22833 Human col
32	790.4	58.1	1066	4	AA157868 Human pol
33	767.4	58.1	806	8	ACC49537 Tumour-as
34	760	57.5	1069	4	AA159654 Human pol
35	755.8	57.2	759	10	ADP17545 Human and
36	755.8	57.2	759	10	ADH62277 Human PME
37	755.8	57.2	759	12	AD039827 Human PME
38	715.4	46.7	878	6	ABK12142 Mouse cDN
39	589.2	44.6	1583	6	AB561424 Prostate
40	493.6	37.4	693	6	ABK12143 Human MIV
41	466.2	35.3	1713	3	AA75152 cDNA enco
42	464.6	35.2	1713	3	AA75167 cDNA clon
43	464.6	35.2	1713	3	AA75166 cDNA clon
44	464.6	35.2	1713	3	AA75168 cDNA clon
45	417.8	31.6	812	2	AA52964 Human pro

## ALIGNMENTS

RESULT 1  
ABK12137 standard; cDNA; 1321 BP.

ABK12137;

05-JUN-2002 (first entry)

Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.  
Human; ss: gene; MIVR-1; Mechanically Induced Vascular Receptor 1;  
cytostatic; cardiant; cerebroprotective; antiarteriosclerotic;  
cardiac cell; anti-apoptotic; vascular endothelial cell;  
cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;  
heart failure.

Homo sapiens.

Key Location/Qualifiers  
CDS 413..1276  
/\*tag= a  
/product= "MIVR-1"  
/note= "This region is specifically claimed in claim 3"

WO200216416-A2.

28-FEB-2002.

21-AUG-2001; 2001WO-US026089.

22-AUG-2000; 2000US-0227159P.

(BGMN) BRIGHAM & WOMEN'S HOSPITAL INC.

(PF12) PFIZER INC.

Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turi TG;

WPI; 2002-280912/32.

P-PSDB; AAU78231.

Novel nucleic acid molecule encoding Mechanically Induced Vascular Receptor-1 polypeptide, useful for treating cardiovascular diseases.

XX Claim 2; Page 87-88; 105bp; English.

PS The invention relates to an isolated nucleic acid molecule encoding a

XX Mechanically induced Vascular Receptor (MIVR)-1 polypeptide having

CC cardiac cell anti-apoptotic activity and fragments of it provided they

CC are not identical to Genbank sequences A1761441.1, A1594390, NM\_004338

CC and A0177461. Also included are expression vectors, host cells, the MIVR-

CC 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting

CC a molecule having cardiac cell anti-apoptotic activity with a candidate

CC agent, where the molecule is a nucleic acid molecule comprising MIVR-1,

CC IEX-1, VDRP-1, BFG-2 and R15-11d or its expression product, determining

CC if the anti-apoptotic activity is modulated and thereby identifying a

CC modulator. The cardiac cell anti-apoptotic molecules and nucleic acids

CC of the invention are useful for treating, diagnosing and monitoring

CC progression of such diseases and disorders as characterised by increased

CC apoptotic cell-death of vascular endothelial cells e.g. cardiac

CC hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart

CC failure. The present sequence encodes human MIVR-1

XX

SQ Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 1321; DB 6; Length 1321;

Best Local Similarity 100.0%; Pred. No. 3e-198;

Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGCGGTCTCGAGCGAAACCGATCTCTTGAGATTGAGAGAGAGAGCGCG 60

DB 1 CGACCGCGGTCTCGAGCGAAACCGATCTCTTGAGATTGAGAGAGAGAGCGCG 60

QY 61 CGGCGCGCGCGCGCGCGCGCGCGCTCGGCGGAGAACTAGCGGCGAGAGCGTCAAGCCC 120

DB 61 CGGCGCGCGCGCGCGCGCGCGCGCTCGGCGGAGAACTAGCGGCGAGAGCGTCAAGCCC 120

QY 121 GCGCGCAGCGCGCGCGCGCGCGCGCGCTCGGCGGAGCGCAAGCGCGGCGCACTGCGCG 180

DB 121 GCGCGCAGCGCGCGCGCGCGCGCGCGCTCGGCGGAGCGCAAGCGCGGCGCACTGCGCG 180

QY 121 GCGCGCAGCGCGCGCGCGCGCGCGCGCTCGGCGGAGCGCAAGCGCGGCGCACTGCGCG 180

DB 121 GCGCGCAGCGCGCGCGCGCGCGCGCGCTCGGCGGAGCGCAAGCGCGGCGCACTGCGCG 180

QY 181 AGCG 240

DB 181 AGCG 240

QY 241 TGAAGCG 300

DB 241 TGAAGCG 300

QY 241 TGAAGCG 300

DB 241 TGAAGCG 300

QY 301 CTCGCCCG 360

DB 301 CTCGCCCG 360

QY 301 CTCGCCCG 360

DB 301 CTCGCCCG 360

QY 361 CCCCG 420

DB 361 CCCCG 420

QY 421 CTTGATGGGGGTCAACAGACCG 480

DB 421 CTTGATGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

QY 481 GTGCAACTGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAAGAGCTGAGATTGTTCA 540

DB 481 GTGCAACTGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAAGAGCTGAGATTGTTCA 540

QY 541 GATCATCATCATCTGT 600

DB 541 GATCATCATCATCTGT 600

QY 541 GATCATCATCATCTGT 600

DB 541 GATCATCATCATCTGT 600

QY 601 CCACACAAAGCTGT 660

DB 601 CCACACAAAGCTGT 660

QY 661 AGATGCTCTGTCTCTGAGAAAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

DB 661 AGATGCTCTGTCTCTGAGAAAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

QY 721 AATCCAGAGCGCGAGGTCTAGCGCCCGGCTCGGCGCCACCGACCGCGCGCGCGCGCG 780

DB 721 AATCCAGAGCGCGAGGTCTAGCGCCCGGCTCGGCGCCACCGACCGCGCGCGCGCGCG 780

QY 781 CTTGCGCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCCACCTATCCGTACCTGAGCAGCA 840

DB 781 CTTGCGCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCCACCTATCCGTACCTGAGCAGCA 840

QY 841 GATGACCTTCCAGCCACCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

DB 841 GATGACCTTCCAGCCACCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

QY 901 CCCCTGACCTTCCAGCTTGT 960

DB 901 CCCCTGACCTTCCAGCTTGT 960

QY 961 GCGGCGACCCCGCAAGACCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020

DB 961 GCGGCGACCCCGCAAGACCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020

QY 1021 CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

DB 1021 CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080

QY 1081 GCGGATGAGAGGCG 1140

DB 1081 GCGGATGAGAGGCG 1140

QY 1141 CTTTCCAGACAGCAG 1200

DB 1141 CTTTCCAGACAGCAG 1200

QY 1201 CACACACATGCGCGCTTGT 1260

DB 1201 CACACACATGCGCGCTTGT 1260

QY 1261 AGGACACCTCTCTTGT 1320

DB 1261 AGGACACCTCTCTTGT 1320

QY 1321 G 1321

DB 1321 G 1321

RESULT 2

ABE22787

ID ABE22787 standard; DNA; 4930 BP.

XX

AC ABE22787;

XX

DT 22-SEP-2005 (first entry)

XX

DE Human colon cancer-associated gene SEQ ID NO:82.

XX

KW cancer; genetic marker; lymphoma; cytostatic; hematological disease;

KW immune disorder; neoplasm; colon tumor; gastrointestinal disease;

KW adenocarcinoma; carcinoma; screening; diagnostic; prognostic;

KW pharmaceutical; ds; gene.

XX

OS Homo sapiens.

XX

PN W02005064009-A1.

PD 14-JUL-2005.

XX

PF 23-DEC-2004; 2004MO-DK000914.

XX

PR 27-DEC-2003; 2003DK-00001940.

PR 24-JAN-2004; 2004DK-0000096.

PR 07-APR-2004; 2004DK-0000086.

PR 26-NOV-2004; 2004DK-00001843.





XX 18-NOV-2004 (first entry)  
DT Tumour-associated antigenic target (TAT) cDNA D3A26860, SEQ ID NO:5823.  
XX  
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
XX tumour; diagnosis; cell proliferative disorder; breast cancer;  
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
XX central nervous system cancer; bladder cancer; pancreatic cancer;  
XX cervical cancer; melanoma; leukemia; hybridisation probe;  
XX chromosome identification; chromosome mapping; gene mapping;  
XX gene therapy; cytostatic; gene; ss.  
OS Homo sapiens.  
XX MO204030615-A2.  
XX  
XX 15-APR-2004.  
XX  
XX 29-SEP-2003; 2003WO-US028547.  
XX  
XX 02-OCT-2002; 2002US-0414971P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Wu TD, Zhang Z, Zhou Y;  
XX WPI, 2004-347921/32.  
XX  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
XX useful in preparing a medicament for treating or detecting a  
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
XX prostate cancer or tumor.  
XX  
XX Claim 1; SEQ ID NO 5823; 7273bp; English.  
XX  
XX The invention relates to human tumour-associated antigenic target (TAT)  
XX polypeptides, and their related nucleic acids. The TAT polypeptides are  
XX overexpressed in cancer tissues compared to normal tissues, and may thus  
XX serve as effective targets for the diagnosis and treatment of cancer in  
XX mammals. The invention also relates to nucleic acid and polypeptide  
XX sequences at least 80% identical to the TAT nucleic acids and  
XX polypeptides; expression vectors and host cells comprising a TAT nucleic  
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic  
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a  
XX TAT polypeptide; and methods and compositions for the treatment or  
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
XX antibodies, antagonists, binding molecules and compositions are useful  
XX for diagnosing or treating a cell proliferative disorder associated with  
XX increased TAT expression, particularly cancers such as breast cancer,  
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
XX cancer, pancreatic cancer, cervical cancer, cancers of the central  
XX nervous system, melanoma and leukemia. TAT nucleic acids may further be  
XX used as hybridisation probes, in chromosome and gene mapping, in  
XX chromosome identification and in gene therapy. The present sequence  
XX represents a TAT nucleic acid of the invention  
XX  
XX Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;  
XX  
XX Query Match 98.5%; Score 1301; DB 13; Length 4911;  
XX Best Local Similarity 100.0%; Pred. No. 3.7e-195;  
XX Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 TGCCAGCCATTTTCCGAGCGCCAGCCCGCGGCACTGCGAGCCGCCCGGCGGCGAG 180  
Qy 201 GGGAGGCGGGGGGGGGCGGAGCGCGGTCCCGGCACTGAGCCCGCGGCGCCCGG 260  
Db 181 GGGAGGCGGGGGGGGGCGGAGCGCGGTCCCGGCACTGAGCCCGCGGCGCCCGG 240  
Qy 261 GAACCTTGCGGCGGAGCCGAGCCCGGAGCGCGGCGCGCTCCCGCGCGCGCTCC 320  
Db 241 GAACCTTGCGGCGGAGCCGAGCCCGGAGCGCGGCGCGCTCCCGCGCGCGCTCC 300  
Qy 321 TGATGCGGGGCGCCCACTCCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCG 380  
Db 301 TGATGCGGGGCGCCCACTCCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCG 360  
Qy 381 CCG 440  
Db 361 CCG 420  
Qy 441 CCG 500  
Db 421 CCG 480  
Qy 501 TGATCCAGAGCATGAGATGACGAGCTGAGTTTGTTCAGATCATCATCATGCTG 560  
Db 481 TGATCCAGAGCATGAGATGACGAGCTGAGTTTGTTCAGATCATCATCATGCTG 540  
Qy 561 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 620  
Db 541 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
Qy 621 GGATCCTTCATCAGCGCGGAGCGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 680  
Db 601 GGATCCTTCATCAGCGCGGAGCGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 660  
Qy 681 GATGCTGTGTCCTCGAGAGCAAGTGTCAAGCAAGCAAGCAAGCAAGCAAGCAAG 740  
Db 661 GATGCTGTGTCCTCGAGAGCAAGTGTCAAGCAAGCAAGCAAGCAAGCAAGCAAG 720  
Qy 741 ACGCGCGCGCTCGGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 800  
Db 721 ACGCGCGCGCTCGGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
Qy 801 TCCAGCGCTTCAGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 860  
Db 781 TCCAGCGCTTCAGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
Qy 861 TCTGCTGTGAGAGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 920  
Db 841 TCTGCTGTGAGAGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900  
Qy 921 GGGAGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 980  
Db 901 GGGAGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 960  
Qy 981 CCATCTTCAGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1040  
Db 961 CCATCTTCAGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1020  
Qy 1041 GTAACTCGGAGCATGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1100  
Db 1021 GTAACTCGGAGCATGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1080  
Qy 1101 CCACCTTACAGGAGGATGATGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1160  
Db 1081 CCACCTTACAGGAGGATGATGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1140  
Qy 1161 GTGGCGCGCGCGCTCTGCTGAGAGGAGCGCGCGCTCCACGACACACATGCGCG 1220  
Db 1141 GTGGCGCGCGCGCTCTGCTGAGAGGAGCGCGCGCTCCACGACACACATGCGCG 1200  
Qy 1221 AGAGCGAGCGCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1280  
Db 1201 AGAGCGAGCGCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

QY 1281 CCCAGGGGGGCTGGGCTGCTAGTGAAGGAGCAG 1321  
DB 1261 CCCAGGGGGGCTGGGCTGCTAGTGAAGGAGCAG 1301

RESULT 4  
ACC49552  
ID ACC49552 standard; cDNA; 4839 BP.  
XX  
AC ACC49552;  
XX  
DT 01-JUL-2003 (first entry)  
XX  
DE Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.  
XX  
KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;  
KW cancer; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003024392-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 11-SEP-2002; 2002MO-US028859.  
XX  
PR 18-SEP-2001; 2001US-0323268P.  
XX  
PR 19-OCT-2001; 2001US-0339227P.  
XX  
PR 07-NOV-2001; 2001US-0336827P.  
XX  
PR 20-NOV-2001; 2001US-0331906P.  
XX  
PR 02-JAN-2002; 2002US-034544P.  
XX  
PR 03-APR-2002; 2002US-0369724P.  
XX  
PR 19-AUG-2002; 2002US-0404809P.  
XX  
PA (GENE) GENENTECH INC.  
XX  
PI Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;  
PI Williams PM, Wu TD, Zhang Z;  
XX  
DR MPI: 2003-354551/3.  
XX  
DR P-PSDB; ABP97234.  
XX  
PT New antibodies against tumor-associated antigenic target polypeptide,  
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.  
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell  
PT carcinomas.  
XX  
PS Claim 2; Fig 119; 285bp; English.  
XX  
CC ACC49493 to ACC49552 encode the human tumour-associated antigenic target  
CC (TAT) proteins given in ABP97175 to ABP97234. The present invention  
CC describes an isolated antibody that binds to a polypeptide having at  
CC least 80 % sequence identity to any of the 60 150-800 residue amino acid  
CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking  
CC its associated signal peptide, encoded by any of the 60 2000-3000 base  
CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have  
CC cytostatic activity. The antibody can be used for treating or diagnosing  
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast  
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal  
CC cell carcinomas, or thyroid cancer.  
XX  
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 8; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 7,2e-184;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAAGCTAGCGGAGGCTCAGCCCGCGGAGCGCGCGCGCTGCGAGCCCAT 152  
DB 1 GGAAAGCTAGCGGAGGCTCAGCCCGCGGAGCGCGCGCGCTGCGAGCCCAT 60  
QY 153 TTCGGAGCGCAGCCCGCGGAGGCTGCGGAGCGCGCGCGCTGCGAGGAGGCGCGG 212

DB 61 TTCGGAGCGCAGCCCGCGGAGGCTGCGGAGCGCGCGCGCTGCGAGGAGGCGCGG 120  
QY 213 GGGCGCAGCGAGAGCGCGCTCCCGGCACTGAGCCCGCGCGCGCGGAACTTGCGCGC 272  
DB 121 GGGCGCAGCGAGAGCGCGCTCCCGGCACTGAGCCCGCGCGCGCGGAACTTGCGCGC 180  
QY 273 GAGCCGAGCCCGCGGAGCGCGCGCTCCCGGCACTGAGCCCGCGCGCGGAACTTGCGCGC 332  
DB 181 GAGCCGAGCCCGCGGAGCGCGCGCTCCCGGCACTGAGCCCGCGCGCGGAACTTGCGCGC 240  
QY 333 CCCAGCTCCGGGCGCGCGCGGAGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392  
DB 241 CCCAGCTCCGGGCGCGCGCGGAGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
QY 393 GCGCGCGCGCGCGCGCGCTTCACTGACCGCTTGATGAGGGGTCAAGACACCGCGCGCGCG 452  
DB 301 GCGCGCGCGCGCGCGCGCTTCACTGACCGCTTGATGAGGGGTCAAGACACCGCGCGCGCG 360  
QY 453 CGCGCGCGCGAGCCCAATGTCCTGCAAGTCACTGCAAGCTTCTTGTTCAGAGCA 512  
DB 361 CGCGCGCGAGCCCAATGTCCTGCAAGTCACTGCAAGCTTCTTGTTCAGAGCA 420  
QY 513 TGGAGATCAGGAGCTGAGATTGTTGTCAGATCATCATCTGAGTGTGATGATGATGA 572  
DB 421 TGGAGATCAGGAGCTGAGATTGTTGTTGTCAGATCATCATCTGAGTGTGATGATGATGA 480  
QY 573 TGGTGTGTGTATATCATGCTGCTGAGCCCTCAAGCTTCTGCAAGCTTCTTCACTCA 632  
DB 481 TGGTGTGTGTATATCATGCTGCTGAGCCCTCAAGCTTCTGCAAGCTTCTTCACTCA 540  
QY 633 GCGCGCAGCGCAGGGGGGAG 692  
DB 541 GCGCGCAGCGCAGGGGGGAG 600  
QY 693 CCTCGAGAGCAGATGTCAAGCAACGGAATCCAGAGCGCGAGCTTACGCCCGCGCTC 752  
DB 601 CCTCGAGAGCAGATGTCAAGCAACGGAATCCAGAGCGCGAGCTTACGCCCGCGCTC 660  
QY 753 GAGCCACGAGCGCGCTGCG 812  
DB 661 GAGCCACGAGCGCGCTGCG 720  
QY 813 AGCCCACTATCCGTAACCTGAGCAGAGATCGAAGCTTCCAGCCCACTCTCGCTGTAG 872  
DB 721 AGCCCACTATCCGTAACCTGAGCAGAGATCGAAGCTTCCAGCCCACTCTCGCTGTAG 780  
QY 873 AGGGGAGAGAGCCCGCACTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 932  
DB 781 AGGGGAGAGAGCCCGCACTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC 840  
QY 933 AGCAGCTGAACTGAACCGGAGATGCGGTGCGCGAGCCCGCAAGAAACATCTTGCACA 992  
DB 841 AGCAGCTGAACTGAACCGGAGATGCGGTGCGCGAGCCCGCAAGAAACATCTTGCACA 900  
QY 993 GTGACCTGATGATGTCAGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCA 1052  
DB 901 GTGACCTGATGATGTCAGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCA 960  
QY 1053 TCAGGCGCAGCTGTAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112  
DB 961 TCAGGCGCAGCTGTAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020  
QY 1113 AGGTATGCGGCACTTACCGCGGCTCTCTTTCAGACCAAGAGCAGTGGCGCGCT 1172  
DB 1021 AGGTATGCGGCACTTACCGCGGCTCTCTTTCAGACCAAGAGCAGTGGCGCGCT 1080  
QY 1173 CTTTCTGAGAGGAGCCCGGCTTCAACACACACATGCGCGCGCTTAGAGAGCGAGCA 1232  
DB 1081 CTTTCTGAGAGGAGCCCGGCTTCAACACACACATGCGCGCGCTTAGAGAGCGAGCA 1140  
QY 1233 TCTGAGCAAGAAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCAAGGGGGGCGC 1292

Db	1141	TCTGGAGCAAAAGAGAAAGATTAACGAAAGACACCCCTCTAGAGGTCCCAAGGGGGGCC	1200
Qy	1293	GGGCTGGGGCTGCGTAGGTGAAAGGACG	1321
Db	1201	GGGCTGGGGCTGCGTAGGTGAAAGGACG	1229
RESULT 5			
ID	ADP65809		
XX	ADP65809	standard; DNA; 4839 BP.	
XX	AC	ADP65809;	
XX	DT	12-AUG-2004 (first entry)	
DE	Human STAG1/PMEP1 mRNA, complete cds	DNA.	
XX			
KW	autoimmune disease; arthritis; gene expression analysis;		
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;		
KW	antiarthritic; osteopatic; antigout; antiinflammatory; dermatological;		
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;		
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;		
KW	immune; de; human.		
XX			
OS	Homo sapiens.		
PN	WO2003072827-A1.		
XX			
PD	04-SEP-2003.		
XX			
PF	31-OCT-2002; 2002MO-US035433.		
PR	31-OCT-2001; 2001US-0336220P.		
XX			
PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.		
PI	Hirsch R, Thornton SL;		
XX			
DR	WPI; 2003-712740/67.		
DR	GENBANK, AF305616.		
XX			
PT	Diagnosing and analyzing autoimmune disease using gene expression		
PT	profiles and microarray technology, useful for diagnosing and treating		
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and		
PT	gout.		
XX			
PS	Disclosure; Page; 56pp; English.		
XX			
CC	The invention relates to a novel method for diagnosing and analysing		
CC	autoimmune disease or arthritides. The method comprises obtaining a		
CC	patient sample containing mRNA, analysing gene expression using the mRNA		
CC	that results in a gene expression signature of the mRNA, and using that		
CC	gene expression signature to diagnose or analyse the autoimmune disease		
CC	or arthritides in the patient, where gene expression of at least 608 of		
CC	the genes correlates with that of the gene signature. The invention		
CC	further comprises a treatment of rheumatoid arthritis, identification of		
CC	genes for targeting in the treatment of rheumatoid arthritis in a mamma		
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mamma; an		
CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or		
CC	analysis of autoimmune disease or rheumatoid arthritis; screening the		
CC	efficacy of a candidate drug in vitro for the treatment of collagen-		
CC	induced arthritis; and reducing the symptoms associated with collagen-		
CC	induced arthritis. The compositions of the invention have the following		
CC	activities: immunosuppressive, antirheumatic, antiarthritic, osteopathi		
CC	c, antigout, antiinflammatory, dermatological, and immunomodulatory. The		
CC	methods and compositions of the present invention are useful for		
CC	diagnosing and treating autoimmune disease or arthritides, such as		
CC	rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,		
CC	fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an		
CC	immune disease caused by an infectious agent. This polynucleotide		
CC	represents a DNA sequence relating to the genes used in the analysis and		
CC	treatment of autoimmune diseases or arthritides. Note: This sequence is		
CC	not shown in the specification. It has been supplied in an electronic		

CC	Format from WIFO.
XX	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
XX	Query Match 93.0%; Score 1229; DB 1; Length 4839;
XX	Best Local Similarity 100.0%; Pred. No. 7.2e-184;
XX	Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	93 GGAAGCTAAGGGCGAGAGGCTCTACCCCGGGGAGAGGCGCGCCGCTCGACAGCCATT 152
DB	1 GGAAAGCTAAGGGCGAGAGGCTCACCCCGGGGAGAGGCGCGCGCCGCTCGACAGCCATT 60
QY	153 TTCCGGAGCGCACC CGCGGAGCACTGCGAGCGCCCCCGGGGCTTGGCGAGAGGGCCGGGG 212
DB	61 TTCCGGAGCGCACC CGCGGAGCACTGCGAGCGCCCCCGGGGCTTGGCGAGAGGGCCGGGG 120
QY	213 GGGCGCAGCGAGAGCGCGTCCCGCGCACTGAGCCCGCGCGGCCCGGGAACTTGGCGGC 272
DB	121 GGGCGCAGCGAGAGCGCGTCCCGCGCACTGAGCCCGCGCGGCCCGGGAACTTGGCGGC 180
QY	273 GACCCGAGCCCGCGGAGCGGGGCGCGCTTCCCGCGCGCGCGCTCTCTGATCGGGGC 332
DB	181 GACCCGAGCCCGCGGAGCGGGGCGCGCTTCCCGCGCGCGCGCTCTCTGATCGGGGC 240
QY	333 CCCAGCTCCGGGGCGCGCGCGGAGCGCCCCCGGGGCGCGCGCGCGCGCGCGCGCG 392
DB	241 CCCAGCTCCGGGGCGCGCGCGGAGCGCCCCCGGGGCGCGCGCGCGCGCGCGCGCG 300
QY	393 GCCGCGCGCGCGCGCGCTCATGACAGCGCTTGATGGGGGCTACAGAGCAGCGCGCGCG 452
DB	301 GCCGCGCGCGCGCGCGCTCATGACAGCGCTTGATGGGGGCTACAGAGCAGCGCGCGCG 360
QY	453 CCGCGCGGCGAGCCCAATGTTCTCTGACAGTGCMACTGCMAACGCTCTTTGTTCCAGAGCA 512
DB	361 CCGCGCGGCGAGCCCAATGTTCTCTGACAGTGCMACTGCMAACGCTCTTTGTTCCAGAGCA 420
QY	513 TGGAGATACAGGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGTGATGATGAGTGA 572
DB	421 TGGAGATACAGGAGCTGGAGTTTGTTCAGATCATCATCATCTGCTGTGATGATGAGTGA 480
QY	573 TGGTGGTGGTATCATCGTGCCTGCTGAGCCACTACAGCTGTCTGACAGCGCTCTTATCA 632
DB	481 TGGTGGTGGTATCATCGTGCCTGCTGAGCCACTACAGCTGTCTGACAGCGCTCTTATCA 540
QY	633 GCCGCGCAGCCAGGGGGGAGAGAGAGAAATGCTCTGTCTTCAGAAAGATGCTGTGGC 692
DB	541 GCCGCGCAGCCAGGGGGGAGAGAGAGAAATGCTCTGTCTTCAGAAAGATGCTGTGGC 600
QY	693 CTTGGAGAGCAAGTGTCAAGGCACGGAATCTCCAGAGCCGAGAGTCTAGCGCCCGCTC 752
DB	601 CTTGGAGAGCAAGTGTCAAGGCACGGAATCTCCAGAGCCGAGAGTCTAGCGCCCGCTC 660
QY	753 GGGCCAGCAGCGAGCTTGCGCGTGCCTTTCGCCAGCGGAGCGCTTTCACCGCTTCC 812
DB	661 GGGCCAGCAGCGAGCTTGCGCGTGCCTTTCGCCAGCGGAGCGCTTTCACCGCTTCC 720
QY	813 AGCCACCTATTCGTAACCTGAGACAAGAGATGACCTTGCACCCACCACTTCGCTGTAG 872
DB	721 AGCCACCTATTCGTAACCTGAGACAAGAGATGACCTTGCACCCACCACTTCGCTGTAG 780
QY	873 AGCGGAGAGAGCCCCACCTTACAGAGGCCCTCTGACCTCTCAGCTTGGGACCCCGAGC 932
DB	781 AGCGGAGAGAGCCCCACCTTACAGAGGCCCTCTGACCTCTCAGCTTGGGACCCCGAGC 840
QY	933 AGCAGCTGAACTGAACCGGGAGTGGGCGGAGCCCGCAAGAGAAACATCTTTCGACA 992
DB	841 AGCAGCTGAACTGAACCGGGAGTGGGCGGAGCCCGCAAGAGAAACATCTTTCGACA 900
QY	993 GTGACCTATGATGTATGATGCTCAGAGCTGGGCGGCGCTTGCAGAGAGAGTACTCGAGCA 1052
DB	901 GTGACCTATGATGTATGATGCTCAGAGCTGGGCGGCGCTTGCAGAGAGAGTACTCGAGCA 960
QY	1053 TAGAGGCCAAGTGTACGGCAGCGGGGCGCATGAGAGGGCGCGCTCCACTTACAGCG 1112

Db 961 TCAGGCCACCTGCTACAGGACGCGCGCGCATGAGAGGCGCGCCGACCTACAGCG 1020  
 Qy 1113 AGGTGATCGGCGACCTACCGCGGGGTCTCTTCCAGCACCGACGAGAGAGTGGCGCCCT 1172  
 Db 1021 AGGTATCGGCGACCTACCGCGGGGTCTCTTCCAGCACCGACGAGAGAGTGGCGCCCT 1080  
 Qy 1173 CTTGCTGAGAGGAGACCGCGCTTCACACACACACATCGCGCCCTTAGAGAGCGAGCA 1232  
 Db 1081 CTTGCTGAGAGGAGACCGCGCTTCACACACACACATCGCGCCCTTAGAGAGCGAGCA 1140  
 Qy 1233 TGTGAGCAAGAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGCGCGC 1292  
 Db 1141 TGTGAGCAAGAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGCGCGC 1200  
 Qy 1293 GGGCTGGGCTGCTGATGTAAGAGGAGC 1321  
 Db 1201 GGGCTGGGCTGCTGATGTAAGAGGAGC 1229  
 RESULT 6  
 ADP65729  
 ID ADP65729 standard; DNA; 4839 BP.  
 AC ADP65729;  
 DT 12-AUG-2004 (first entry)  
 DE Human transmembrane, prostate androgen induced RNA (TMEMPA1), DNA.  
 KM autoimmune disease; arthritis; gene expression analysis;  
 KM rheumatoid arthritis; collagen-induced; immunosuppressive; antineumatic;  
 KM antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
 KM immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
 KM fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KM immune; ds; human.  
 OS Homo sapiens.  
 PN MO2003072827-A1.  
 PD 04-SEP-2003.  
 PF 31-OCT-2002; 2002MO-US035433.  
 PR 31-OCT-2001; 2001US-0336220P.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PI Hirsch R, Thornton SL;  
 DR WPI; 2003-712740/67.  
 DR GENBANK; NM\_020182.  
 PT Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.  
 PS Disclosure; Page; 56pp; English.  
 CC The invention relates to a novel method for diagnosing and analyzing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analyzing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antineumatic, antiarthritic, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC method and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This polynucleotide  
 CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.  
 SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;  
 Query Match 93.0%; Score 1229; DB 11; Length 4839;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-184;  
 Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 93 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCCCGTGCACGCCATT 152  
 Db 1 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCCCGTGCACGCCATT 60  
 Qy 153 TTCCGAGAGCCACCCCGCGGAGCTGCGAGCGCCCGCGGAGCGGAGCGCGG 212  
 Db 61 TTCCGAGAGCCACCCCGCGGAGCTGCGAGCGCCCGCGGAGCGGAGCGCGG 120  
 Qy 213 GGGCGAGCGAGCGGCTCCCGGCACTGAGCCCGCGGCGCGCCCGGAACTTGGCGGC 272  
 Db 121 GGGCGAGCGAGCGGCTCCCGGCACTGAGCCCGCGGCGCGCCCGGAACTTGGCGGC 180  
 Qy 273 GACCCGAGCCCGCGGAGCGCGGCGCGCTCCCGCGCGCGCTCTTCGATGCGGCGC 332  
 Db 181 GACCCGAGCCCGCGGAGCGCGGCGCGCTCCCGCGCGCGCTCTTCGATGCGGCGC 240  
 Qy 333 CCCAGCTCCGGGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 392  
 Db 241 CCCAGCTCCGGGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 300  
 Qy 393 GCCGCGCGCGCGCGCGCTGCATGCAACCGCTTATGAGGAGTCAACAGCACCGCGCGCG 452  
 Db 301 GCCGCGCGCGCGCGCGCTGCATGCAACCGCTTATGAGGAGTCAACAGCACCGCGCGCG 360  
 Qy 453 CCGCGCGCGAGCCCAATGCTCTGCACTGCACTGCAAAAGCTTTGTTCCAGAGCA 512  
 Db 361 CCGCGCGCGAGCCCAATGCTCTGCACTGCACTGCAAAAGCTTTGTTCCAGAGCA 420  
 Qy 513 TGGAGATCAGGAGCTGAGATTTGTTCAAGATCATCATGCTGAGATGATGATGTA 572  
 Db 421 TGGAGATCAGGAGCTGAGATTTGTTCAAGATCATCATGCTGAGATGATGATGTA 480  
 Qy 573 TGGTGTGTATGATGATGCTGCTGAGCACTAACAAGTGTCTGACAGTCTTCATCA 632  
 Db 481 TGGTGTGTATGATGATGCTGCTGAGCACTAACAAGTGTCTGACAGTCTTCATCA 540  
 Qy 633 GCCGAGCAAGCGGAGGAGAGAGAGAAATGCTGTCTCAGAGAGATCCTGTGGC 692  
 Db 541 GCCGAGCAAGCGGAGGAGAGAGAGAAATGCTGTCTCAGAGAGATCCTGTGGC 600  
 Qy 693 CTTGAGAGAGCACTGTGTCAGGCAACGGAATCCAGACCGGAGGTCTACCGCGCGCTC 752  
 Db 601 CTTGAGAGAGCACTGTGTCAGGCAACGGAATCCAGACCGGAGGTCTACCGCGCGCTC 660  
 Qy 753 GGGCCACGAGCGGCTGCGCGGCGCGCTTGCAGCGGAGAGGCTTCCACCGCTTC 812  
 Db 661 GGGCCACGAGCGGCTGCGCGGCGCGCTTGCAGCGGAGAGGCTTCCACCGCTTC 720  
 Qy 813 AGCCACCTATCGTACCTGAGACAGAGATGACCTTCCACCACTTCGCTGTAG 872  
 Db 721 AGCCACCTATCGTACCTGAGACAGAGATGACCTTCCACCACTTCGCTGTAG 780









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QY 573 TGGTGTGTGTATCATCGTGTCTGCTGAGCCACTACAGACTGTCTGCAAGCGTCTTCATCA 632
DB 481 TGGTGTGTGTATCATCGTGTCTGCTGAGCCACTACAGACTGTCTGCAAGCGTCTTCATCA 540
QY 633 GCCGGCAGCGAGCGGGGCGAGAGAGAAAGATGCGCTCTCTCCAGAAAGATGCGGTGGC 692
DB 541 GCCGGCAGCGAGCGGGGCGAGAGAGAAAGATGCGCTCTCTCCAGAAAGATGCGGTGGC 600
QY 693 CCTCGAGAGCAGCATGTCTCAGGCAACGGAATCCAGAGCCGCAAGGTCTAGCGCCCGCTC 752
DB 601 CCTCGAGAGCAGCATGTCTCAGGCAACGGAATCCAGAGCCGCAAGGTCTAGCGCCCGCTC 660
QY 753 GGGCCACCGACCGCTGGCGCGCTGCGCCCTTTCGCCACCGGAGAGGCTTCCACCGCTTCC 812
DB 661 GGGCCACCGACCGCTGGCGCGCTGCGCCCTTTCGCCACCGGAGAGGCTTCCACCGCTTCC 720
QY 813 AGCCCACTATCCGTAACCTGACAGCAGAGATGCACTTGCACCCACATCTCGCTGTAG 872
DB 721 AGCCCACTATCCGTAACCTGACAGCAGAGATGCACTTGCACCCACATCTCGCTGTAG 780
QY 873 AGGGGAGAGAGCGCCCACTTACAGAGGCGCCCTGCAACCTTCAGCTTGGGAGCCCGAGC 932
DB 781 AGGGGAGAGAGCGCCCACTTACAGAGGCGCCCTGCAACCTTCAGCTTGGGAGCCCGAGC 840
QY 933 AGCAGCTGGAATCTGAACCGGAGAGTGTGTGCGGCAACCCCAAGAAACATCTTCCACA 992
DB 841 AGCAGCTGGAATCTGAACCGGAGAGTGTGTGCGGCAACCCCAAGAAACATCTTCCACA 900
QY 993 GTGACCTGATGGAATGTCGACAGGCTGGGCGGCGCCCTGCGCCCGCAGAGTAATCGAGCA 1052
DB 901 GTGACCTGATGGAATGTCGACAGGCTGGGCGGCGCCCTGCGCCCGCAGAGTAATCGAGCA 960
QY 1053 TCAGGCGCAAGTGTCTACAGCAGCGGCGGCGGCGATGAGAGGCGCGCCCACTTACAGCG 1112
DB 961 TCAGGCGCAAGTGTCTACAGCAGCGGCGGCGGCGATGAGAGGCGCGCCCACTTACAGCG 1020
QY 1113 AGGTATATGGCCACTAACCCGGGGTCTCTCTTTCAGACCAAGACAGAGTGCGCGCTCT 1172
DB 1021 AGGTATATGGCCACTAACCCGGGGTCTCTCTTTCAGACCAAGACAGAGTGCGCGCTCT 1080
QY 1173 CCTTGTGAGGAGGAGCGCGGCTCCACACACACATGCGCCCTTAGAGAGCGAGCCA 1232
DB 1081 CCTTGTGAGGAGGAGCGCGGCTCCACACACACATGCGCCCTTAGAGAGCGAGCCA 1140
QY 1233 TCTGAGAGCAAGAGAGATTAACAGAAAGAGACACCTCTCTTAGGGTCCCAAGGGGGCC 1292
DB 1141 TCTGAGAGCAAGAGAGATTAACAGAAAGAGACACCTCTCTTAGGGTCCCAAGGGGGCC 1200
QY 1293 GGGCTGGGGCTGCGTATGTTGAAAAAGCGAG 1321
DB 1201 GGGCTGGGGCTGCGTATGTTGAAAAAGCGAG 1229

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RESULT 9  
ADR66778  
ID ADR66778 standard; DNA; 4839 BP.

AC ADR66778;

DT 02-DEC-2004 (first entry)

XX Human prostatic carcinoma derived DNA SEQ ID 71 #4.

XX human; cytostatic; diagnosis; prostatic cancer;

XX differential expression analysis; ds.

OS Homo sapiens.

PN WO2004076614-A2.

PD 10-SEP-2004.

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PF 22-FEB-2004; 2004WO-DE000433.
XX 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PIL/) PILARSKY C.
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T,
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S,
PI Xinzhong L, Staub E,
XX WPI; 2004-653386/63.
XX
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
XX Claim 1; Page 1447; 1607pp; German.
XX
XX This invention describes novel cytostatic polynucleotide and polypeptide
XX sequences which can be used in a method for diagnosing prostatic cancer
XX or the risk of developing prostatic cancer. Diagnosis is based on
XX determining over transcription or over expression of the sequences in
XX prostatic tissue. Screening for inhibitors of the sequences or detection
XX substances involves a binding assay; any compounds that bind are
XX selected, optionally after deconvolution of mixtures. Detection of a
XX predetermined minimum level of the reporter indicates the presence of
XX tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX short-interfering RNA or ribozymes; an organic molecule of molecular
XX weight below 5000, preferably 300, that binds to the polypeptide; an
XX aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
XX polypeptide, preferably humanised or human; an anti-idiotypic, non-human
XX (monoclonal) antibody directed against Ab or any of the above derivatised
XX with a reporter group, cell toxin, immunostimulatory molecules and/or
XX radioisotope. The polynucleotides are identified in human prostatic
XX cancer by differential expression analysis, using DNA microarrays,
XX between normal and tumorous tissues, with (over)expression being detected
XX by quantitative PCR. Analysis of prostatic cancer samples showed that
XX CD24 was upregulated in many of them. Sections of tissue, isolated from
XX prostatic cancer patients, or subjects at risk, were incubated
XX sequentially with anti-human CD4 murine monoclonal antibodies;
XX biotinylated second antibody; streptavidin-conjugated horseradish
XX peroxidase and then diaminobenzidine as colour former (brown). The
XX samples were counterstained with hemalum (blue). Malignant cells stained
XX strongly but non-malignant cells only weakly. In 15 of 63 samples of
XX adenocarcinoma, membrane and cytoplasmic staining was very strong, and
XX lymph node metastases were also stained. ADR65805-ADR6654 represent the
XX polynucleotide and polypeptide sequences used in the method of the
XX invention.
XX
XX Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
SQ
XX
XX Query Match 93.0%; Score 1229; DB 13; Length 4839;
XX Best Local Similarity 100.0%; Pred. No. 7, 2e-184;
XX Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCGGGGAGAGCGGCGCGCTGCGAGCCATT 152
DB 1 GGAAGCTAGCGGAGAGGCTCAGCCCGGGGAGAGCGGCGCGCTGCGAGCCATT 60
QY 153 TTCCGAGCGCCACCGCGGGGCACTGCGAGCGCCCGGGGCTGCGAGGGAGAGCGCGGG 212
DB 61 TTCCGAGCGCCACCGCGGGGCACTGCGAGCGCCCGGGGCTGCGAGGGAGAGCGCGGG 120
QY 213 GGGGCGAGCGGAGCGGCTCCCGGCACTGAGCCCGCGGCGCGCGGAACTTTGGCGGC 272
DB 121 GGGGCGAGCGGAGCGGCTCCCGGCACTGAGCCCGCGGCGCGCGGAACTTTGGCGGC 180
QY 273 GACCCGAGCGCGGAGCGGCGGCGCGCTCCCGCGCGCGCGCTCTGATGCGGGGC 332

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[illegible]

ID	ADU06063	standard; DNA; 4839 BP.
AC	ADU06063;	
DT	27-JAN-2005	(first entry)
DE	Novel bronchial cancer-associated human gene SeqID285.	
KM	bronchial cancer; cytostatic; tumour-associated protein;	
KW	cancer detection; metastasis; tumour; gene; ds; human.	
OS	Homo sapiens.	
XX	DEI0316701-A1.	
PD	04-NOV-2004.	
PF	09-APR-2003; 2003DE-01016701.	
PR	09-APR-2003; 2003DE-01016701.	
PA	(HINZ/) HINZMANN B.	
PA	(HERM/) HERMANN K.	
XX	(CAST/) HEIDEN CASTANOS-VELEZ E.	
P1	Mennrich D, Brumendorf T, Heiden E, Hermann K, Kinemann H;	
P1	Li X, Roepcke S, Staud E, Hinzmam B, Rosenthal A, Pilarsky C;	
DR	WPI; 2004-786403/78.	
PS	P-PSDB; ADU06550.	
PT	New nucleic acid, and derived proteins, useful for diagnosis of bronchial	
PT	cancer and in screening for therapeutic and diagnostic agents.	
XX	Claim 1; SEQ ID NO 285; 1381bp; German.	
XX	This invention relates to a novel isolated nucleic acid associated with	
CC	bronchial cancer comprising 489 defined sequences given in the	
CC	specification. The invention may be useful for the production of	
CC	compounds with a cytostatic activity through the inhibition of expression	
CC	or activity of tumour-associated proteins. The novel DNA sequences and	
CC	the proteins/peptides encoded by them are used for detecting bronchial	
CC	cancer or determining the risk of developing it and to screen for	
CC	specific binding partners of the DNA or protein sequences, where the	
CC	binding partners are potentially useful as agents for treating or	
CC	diagnosing bronchial cancer. The DNA or protein sequences can also be	
CC	used for prognosis, detection of metastases, and for secondary treatment	
CC	(of tumours that have been stabilised or are no longer detectable).	
CC	Detecting abnormal expression of the DNA sequences provides early	
CC	diagnosis of bronchial cancers. The present sequence is that of a novel	
CC	bronchial cancer-associated human gene sequence of the invention.	
XX	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;	
QY	Query Match	93.0%; Score 1229; DB 13; Length 4839;
Db	Best Local Similarity	100.0%; Pred. No. 7,2e-184;
Matches 1229;	Conservative	0; Mismatches 0; Indels 0; Gaps 0
93	GGAAGCTAGCGGCAAGAGCTCAGGCCCGCGGCGAGCGCGCCCGCTGCACGCCCATTT	152
1	GGAAACTAGCGGCAAGAGCTCAGGCCCGCGGCGAGCGCGCCCGCTGCACGCCCATTT	60
153	TTCGCGAGCGCACCGCGGCGCACTGCGCAGCGCCCCCGGGGCTTGCAGAGGGAGAGCCGGG	212
61	TTCGCGAGCGCACCGCGGCGCACTGCGCAGCGCCCCCGGGGCTTGCAGAGGGAGAGCCGGG	120
213	GGGCGAGGCGGAGCGCGGTCCCGCGCATGAGCGCCCGCGGCGCGGGAATTGGCGGC	272
121	GGGCGAGGCGGAGCGCGGTCCCGCGCATGAGCGCCCGCGGCGCGGGAATTGGCGGC	180
273	GACCCGAGCGCGGCGAGCGCGGGGCGGCTCCCGCGCGCGCGCTTGTCATGCGCGGC	332

Db	181	GACCCGAGCCCGGCGAGCGCCGGGGCGCGGCTCCCCCGCGCGCGCTCTCGATGAGGGAGC	240
QY	333	CCGAGCTCCGGAGCGCCGGCCGAGACCCCCCGCGCGCTCCCGAGCCCCCGCGCCCGC	392
Db	241	CCGAGCTCCGGAGCGCGGAGCGGAGGCCCCCGCGCGCTCCCGAGCCCCCGCGCCCGC	300
QY	393	GGCGCGCGCGCGCGCGCTGCATGTGACCGGCTTGATGGGGGTCAACAGCACCGCGCGCG	452
Db	301	GGCGCGCGCGCGCGCTGCATGTGACCGCTTGATGGGGGTCAACAGCACCGCGCGCG	360
QY	453	CCGCGGGGAGCCCAATGTCCTCGACAGTGCACCTGCMAACGCTCTTTGTTTCAGAGCA	512
Db	361	CCGCGGGGAGCCCAATGTCCTCGACAGTGCACCTGCMAACGCTCTTTGTTTCAGAGCA	420
QY	513	TGGAGATCACGAGAGCTGGAGTTTGTTCAGATCATCATCTGTGTGTGATGATGTGA	572
Db	421	TGGAGATCACGAGAGCTGGAGTTTGTTCAGATCATCATCTGTGTGTGATGATGTGA	480
QY	573	TGGAGTGTGTATCACGTCGCTGAGCACCTACACGTCGTGACAGGCTCTTCATCA	632
Db	481	TGGTGTGTGTATCACGTCGCTGAGCACCTACACGTCGTGACAGGCTCTTCATCA	540
QY	633	GCCGCGACAGCCAGGGGCGAGAGAGAGATGCCCCGTGCTCAGAAAGATGCCGTGGC	692
Db	541	GCCGCGACAGCCAGGGGCGAGAGAGAGATGCCCCGTGCTCAGAAAGATGCCGTGGC	600
QY	693	CCTCGGAGAGACACAGTGTACGAGCCAAACGGAATCCAGAGCCGACGATCAAGCCCCGCTC	752
Db	601	CCTCGGAGAGACACAGTGTGTAGGAGCAACGGAATCCAGAGCCGAGGTCATAGCCCCGCTC	660
QY	753	GAGCCACAGCAGCGCTGCGCGCTGCGCCCTTCGCCCAGCGGAGAGCGCTTCACCGCTTC	812
Db	661	GAGCCACAGCAGCGCTGCGCGCTGCGCCCTTCGCCCAGCGGAGAGCGCTTCACCGCTTC	720
QY	813	AGCCCACTATTCGTAACCTGCGACGAGAGTGAACCTGCGACCCACATCTCGCTGTAG	872
Db	721	AGCCCACTATTCGTAACCTGCGACGAGAGTGAACCTGCGACCCACATCTCGCTGTAG	780
QY	873	ACGGGGAAGAGCCCCACCCCTACACAGGGGCCCTGACCTTCAGCTTGGGAGCCCGAGC	932
Db	781	ACGGGGAAGAGCCCCACCCCTACACAGGGGCCCTTCAGCTTGGGAGCCCGAGC	840
QY	933	AGCAGCTGAACTGAAACCGGGAGTGTGATGCGGCAACCCCAACGAACATCTTCGACA	992
Db	841	AGCAGCTGAACTGAAACCGGGAGTGTGATGCGGCAACCCCAACGAACATCTTCGACA	900
QY	993	GTCACCTGATGATATGTGCGACGACTGGGCGGCTGCGCCCCCGACAGTAACTCGGGCA	1053
Db	901	GTCACCTGATGATATGTGCGACGACTGGGCGGCGCTGCGCCCCCGACAGTAACTCGGGCA	960
QY	1053	TCAGGGCCACGTCATACGAGCAGCGGCGGAGCGCATGAGGGGGCGCGGCCACTACAGC	1112
Db	961	TCAGGGCCACGTCATACGAGCAGCGGCGGAGCGCATGAGGGGGCGCGGCCACTACAGC	1020
QY	1113	AGGTGATCGGCCACTACCCGGGGTCTCTCTTCAGACACGACGAGCAGTGGGCGGCTT	1172
Db	1021	AGGTGATCGGCCACTACCCGGGGTCTCTCTTCAGACACGAGGAGCAGTGGGCGGCTT	1080
QY	1173	CCTTGCTGAGAGGGGACCGGGCTCCACACACACATGCGCGCCCTTAAGAGCGGAGCA	1233
Db	1081	CCTTGCTGAGAGGGGACCGGGCTCCACACACACATGCGCGCCCTTAAGAGCGGAGCA	1140
QY	1233	TCTGAGCAAAAGAGAGATAAACAGAAAGACACCTCTCTAGAGGTCCCGCAGGGGGCC	1292
Db	1141	TCTGAGCAAAAGAGAGATAAACAGAAAGACACCTCTCTAGAGGTCCCGCAGGGGGCC	1200
QY	1293	GGGCTGGGGCTGCTGATGGTGAAGGCGAG	1321
Db	1201	GGGCTGGGGCTGCTGATGGTGAAGGCGAG	1229

RESULT 11  
ADW43368

ID	ADM43368 standard; DNA; 4839 BP.
XX	
AC	ADM43368;
XX	
DT	24-MAR-2005 (first entry)
XX	
DE	Prostate cancer related gene, SEQ ID 166.
XX	
KW	Cytostatic; Gene Therapy; Prostate tumor; prostatic cancer; diagnosis; ds; gene.
OS	Homo sapiens.
XX	
FN	WO2004113571-A2.
PD	
XX	
PE	25-JUN-2004; 2004WO-IB002394.
XX	
PR	26-JUN-2003; 2003US-0482595P.
XX	
PA	(EXON-) EXONHIT THERAPEUTICS SA.
XX	
PI	Einstein R, McGowan KM, Pando MP;
DR	WPI; 2005-057996/06.
XX	
PT	New isolated nucleic acid sequence that is expressed by human prostate cancer cells, useful as target for treating, preventing and/or diagnosing cancers, particularly prostate cancer.
PT	
PS	Claim 1; SEQ ID NO 166; 198pp; English.
XX	
CC	The present invention relates to novel nucleic acid sequences that are expressed by human prostate cancer cells. The nucleic acid sequences or the encoded proteins are useful as targets for treating, preventing and/or diagnosing cancers, particularly prostate cancer. The present sequence is one such nucleic acid of the invention.
CC	
CC	
SQ	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
Query Match	93.0%; Score 1229; DB 14; Length 4839;
Best Local Similarity	100.0%; Pred. No. 7.2e-184;
Matches 1229; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
DG	
OY	93 GGAAAGCTAAGGGGAGAGGCTCAGCCCCCGGGGAGAGCCGCCGTGCAGGCCATT 152       1 GGAAAGCTAAGGGGAGAGGCTCAGCCCCCGGGGAGAGCCGCCGTGCAGGCCATT 60
DG	
OY	153 TTCCGAGACGCACC CGCGGAGCATGCGCACGCCCCCGGGGCTGCGGAGGAGAGCCGGGG 212       61 TTCGGAGAGCAACCGCGGGGATGCGGACGAGCCCCCGGGGCTGCGGAGGAGGCGGGGG 120
DG	
OY	213 GGGCGAGCGAGAGCGCGGTCCC CGGCACTTGAAGCCCCCGGGGCGCCCGGGAAACTTGCGCGC 272       121 GGGCGAGCGAGAGCGCGGTCCC CGGCACTTGAAGCCCCCGGGGCGCCCGGGAAACTTGCGCGC 180
DG	
OY	213 GAGCCGAGACCCCGGAGAGCGCGGGGCGGCGTCCCCCGCGCGCGGCGCTCTGCAATGCGGGGC 332       181 GAGCCGAGACCCCGGAGAGCGCGGGGCGGCGTCCCCCGCGCGCGGCGCTCTGCAATGCGGGGC 240
DG	
OY	333 CCAGAAGCTCCGGAGCGCGGCGCGAGAGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 392       241 CCAGAAGCTCCGGAGCGCGGCGCGAGAGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 300
DG	
OY	393 GCCGCGCGCGCGCGCGCTGTCATATGACCGCTTGATGGGGGTCAAACGACACCGCGCGCGCGC 452       301 GCCGCGCGCGCGCGCGCTGTCATATGACCGCTTGATGGGGGTCAAACGACACCGCGCGCGCGC 360
DG	
OY	453 CCGCGCGCGAGCGCCCAATGTCTCTGAGAGTGCATAATTGAAAGCGCTTTGTTCCAGAGACA 512       361 CCGCGCGCGAGCGCCCAATGTCTCTGAGAGTGCATAATTGAAAGCGCTTTGTTGTCAGAGACA 420

OY	513	TGAGATCACGSACCTGGATTGTTCAGATCATCATCATCATGATGATGATGATGGA	572
Dd	421	TGGAGATCACGSACTGGAGTTTGTTCAGATCATCATCATCATGATGATGATGGA	480
OY	573	TGATGTGTGTATCAGCTGCCTGTGCACCATAAAGCTGTCTTGACAAGTCTTCATCA	632
Dd	481	TGATGTGTGTATCAGCTGCCTGTGCACCATAAAGCTGTCTTGACAAGTCTTCATCA	540
OY	633	GCCGGCACAGCCAGAGGGGGGAGAGAGAAGATGCCCTGTCTTCAGAAAGATGCTGTGGC	692
Dd	541	GCCGGCACAGCCAGAGGGGGGAGAGAGAAGATGCCCTGTCTTCAGAAAGATGCTGTGGC	600
OY	693	CCTGGAGAGACAGTGTCAAGSCAACAGAAATCCCAGAGCCGACGGTCAACGCCCGGCTC	752
Dd	601	CCTGGAGAGACAGTGTCAAGSCAACAGAAATCCCAGAGCCGACGGTCAACGCCCGGCTC	660
OY	753	GGCCCCACGACCGGCTGTGGCCGTGCCGCTTCGCCCCAGCGGAGAGCGCTTCACCGCTTCC	812
Dd	661	GGCCCCACGACCGGCTGTGGCCGTGCCGCTTCGCCCCAGCGGAGAGCGCTTCACCGCTTCC	720
OY	813	AGCCCACTTATCCGTACTCTGCAGCACAGAGATCGAATCTTGCCACCCACATATCTCGCTGTAG	872
Dd	721	AGCCCACTTATCCGTACTCTGCAGCACAGAGATCGAATCTTGCCACCCACATATCTCGCTGTAG	780
OY	873	ACGGGAGAGAACCCCCACCTTAACAGGAGCCCTGTGACCTCCAGCTTGTGGAGCCCGAGC	932
Dd	781	ACGGGAGAGAACCCCCACCTTAACAGGAGCCCTGTGACCTCCAGCTTGTGGAGCCCGAGC	840
OY	933	AGCAGCTGGAATGAACTGAACCGGGAGTGTGGTGGCGGCACCCCCAAACGAACATCTTTCAGCA	992
Dd	841	AGCAGCTGGAATGGAATGAACTGAACCGGGAGTGTGGTGGCGGCACCCCCAAACGAACATCTTTCAGCA	900
OY	993	GTAACCTGATGGAATGATGTCACAGGCTGGGGGGGCCCTGTGCCCCCCAGCAGTAACTGGGACA	1052
Dd	901	GTAACCTGATGGAATGATGTCACAGGCTGGGGGGGCCCTGTGCCCCCCAGCAGTAACTGGGACA	960
OY	1053	TCAGGCGCACGTCCTTACGCGACGCGGCGGGCGAGCTGAAGGGGGCGCGGCCCTTACAGCG	1112
Dd	961	TCAGGCGCACGTCCTTACGCGACGCGGCGGGCGAGCTGAAGGGGGCGCGGCCCTTACAGCG	1020
OY	1113	AGGTATATGGGCACTAACCCGGGGGTCTCTTTCACACACAGTAGAGCATGTGGGCCGCCCT	1172
Dd	1021	AGGTATATGGGCACTAACCCGGGGGTCTCTTTCACACACAGTAGAGCATGTGGGCCGCCCT	1080
OY	1173	CCTTGCTGAGAGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA	1232
Dd	1081	CCTTGCTGAGAGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA	1144
OY	1233	TCTGAGCAGAAAGAGAGATTAACAGAAAGACACCTCTTCTTAGGGGTCCCGAGGGGGGCC	1292
Dd	1141	TCTGAGCAGAAAGAGAGATTAACAGAAAGACACCTCTTCTTAGGGGTCCCGAGGGGGGCC	1200
OY	1293	GGGCTGGGGCTCCGTATAGTGAAGAAAGCAG	1321
Dd	1201	GGGCTGGGGCTCCGTATAGTGAAGAAAGCAG	1229

AD	RESULT 12
AD	ADGC37326
ID	ADGC37326 standard; DNA; 1383 BP.
XX	
AC	ADGC37326;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.
XX	
KM	Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KM	cancer; infectious disease; bone disease; AIDS;
KM	neurodegenerative disease; ischemic disorder; AntiInflammatory;
KM	immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KM	Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds
XX	

OS	Homu sapiens.
XX	
PN	WO2003048202-A2.
PD	
XX	12-JUN-2003.
XX	
PF	03-DEC-2002; 2002WO-JP012644.
XX	
PR	03-DEC-2001; 2001JP-00368692.
PR	05-DEC-2001; 2001US-0335829P.
PR	03-OCT-2002; 2002JP-00281302.
PR	04-OCT-2002; 2002US-0415769P.
XX	
PA	(ASAH ) ASAMI KASEI KK.
XX	
PI	Matsuda A, Muramatsu S;
XX	
DR	WPI, 2003-505282/47.
DR	P-PSDB; ADC37327.
XX	
PT	New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT	useful for treating inflammation, autoimmune diseases, cancers,
PT	infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT	ischemic disorders.
XX	
PS	Claim 4; SEQ ID NO 159; 938pp; English.
XX	
CC	The present invention relates to novel proteins and their coding
CC	sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC	kappaB). The proteins and their coding sequences are useful for treating
CC	a disease associated with NF-kappaB activation, such as inflammation,
CC	autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC	neurodegenerative diseases, or ischemic disorders.
XX	
SO	Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;

Query Match	Similarity	92.9%	Score 1227.4	DB 10	Length 1383
Best Local	Similarity	99.9%	Pred. No. 1.4e-183		
Matches 1228	Conservative	0	Mismatches 1	Indels 0	Gaps 0
QY	93	GGAAAGCTAGCGGCGAGAGGCTTCAGCCCGGCGGCGAGCGCGCGCCCGCTGCAGGCCATT	152		
Db	1	GGAAAGCTAGCGGCGAGAGGCTTCAGCCCGGCGGCGAGCGCGCGCCCGCTGCAGGCCATT	60		
QY	153	TTCCGGAAGCCACCCGCGGCGCACTGCGCAGCGCCCCCGGGGCTGCGAGGGGAGGCGCGGGG	212		
Db	61	TTCCGGAAGCCACCCGCGGCGCACTGCGCAGCGCCCCCGGGGCTGCGAGGGGAGGCGCGGGG	120		
QY	213	GGGCGCGAGCGGAGCGCGGCTCCCGCGCACTGAACCGCGGCGCGCCCGGGGACTTGGCGGC	272		
Db	121	GGGCGCGAGCGGAGCGCGGCTCCCGCGCACTGAACCGCGGCGCGCCCGGGGACTTGGCGGC	180		
QY	273	GACCGGAGCGCGGCGAGCGCGGCGCGCTCCCGCGCGCGCGCTCTTGATGCGGGGCG	332		
Db	181	GACCGGAGCGCGGCGAGCGCGGCGCGCTCCCGCGCGCGCGCTCTTGATGCGGGGCG	240		
QY	333	CCGAGCTCCGGGCGCGCGCGGAGCTCCCGCGCGCGCCCGAGGCCCCCGCGCTCGC	392		
Db	241	CCGAGCTCCGGGCGCGCGCGGAGCTCCCGCGCGCGCCCGAGGCCCCCGCGCTCGC	300		
QY	393	GCGCGCGCGCGCGCGCGCTTCATGCAACCGTTATGGGGGTCAACAGCACCGCGCGCGCG	452		
Db	301	GCGCGCGCGCGCGCGCGCTTCATGCAACCGTTATGGGGGTCAACAGCACCGCGCGCGCG	360		
QY	453	CGCGCGGCGAGCGCCATGCTCTCTTGACGTGCACTGCAACCGCTTTTGTTCAGAGCA	512		
Db	361	CGCGCGGCGAGCGCCATGCTCTCTTGACGTGCACTGCAACCGCTTTTGTTCAGAGCA	420		
QY	513	TGAGATCACGAGCTGAGCTTGTTCATATCATCATCTGCTGGTGGTGAATGATGCTGA	572		
Db	421	TGAGATCACGAGCTGAGCTTGTTCATATCATCATCTGCTGGTGGTGAATGATGCTGA	480		
QY	573	TGCTGTGTGATTCACGTGCTCTGAGGCACTACAGCTGTCTGCAAGGCTCTTCATCA	632		







QY 773 GTGCGGCGCTTGCGCCAGGAGGCGCTTCCAGCGCTTCCAGCCCACTATCCGACTG 832  
 XX |||||  
 Db 361 GTGCGGCGCTTGCGCCAGGAGGCGCTTCCAGCGCTTCCAGCCCACTATCCGACTG 420  
 XX |||||  
 QY 833 CAGCAGGATGACCTGCAACCCACCATCTGCTGTGACAGCGGGAGAGCCCCCAACC 892  
 XX |||||  
 Db 421 CAGCAGGATGACCTGCAACCCACCATCTGCTGTGACAGCGGGAGAGCCCCCAACC 480  
 XX |||||  
 QY 893 TACCAAGGCGCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTG 952  
 XX |||||  
 Db 481 TACCAAGGCGCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTG 540  
 XX |||||  
 QY 953 GAGTGGTGGCGGCGACCCCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1012  
 XX |||||  
 Db 541 GAGTGGTGGCGGCGACCCCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 600  
 XX |||||  
 QY 1013 AGGCTGGGCGGCGCTGCGCCCGCCAGAGTAAGTGGGCGATCAGCGCCAGCTGACGCG 1072  
 XX |||||  
 Db 601 AGGCTGGGCGGCGCTGCGCCCGCCAGAGTAAGTGGGCGATCAGCGCCAGCTGACGCG 660  
 XX |||||  
 QY 1073 AGCGGCGGCGCGATGAGAGGCGCGCGCCGACCTTACAGGAGGTGATGCGCACTACCG 1132  
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 Db 661 AGCGGCGGCGCGATGAGAGGCGCGCGCCGACCTTACAGGAGGTGATGCGCACTACCG 720  
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 QY 1133 GGGTCTCTCTTCCAGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1192  
 XX |||||  
 Db 721 GGGTCTCTCTTCCAGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
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 QY 1193 CTCACACACACACATGCGCGCCCTTAGAGAGCGGCAATCTGGAGCAAGAGAGAT 1252  
 XX |||||  
 Db 781 CTCACACACACACATGCGCGCCCTTAGAGAGCGGCAATCTGGAGCAAGAGAGAT 840  
 XX |||||  
 QY 1253 AACGAGAAAGACACCTCTCTAG 1276  
 XX |||||  
 Db 841 AACGAGAAAGACACCTCTCTAG 864  
 XX |||||

## RESULT 15

ID AAA75151 standard; CDNA; 969 BP.  
 AC AAA75151;

DT 15-JAN-2001 (first entry)  
 DE

CDNA encoding a human TANGO 261 polypeptide.

TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;  
 cellular proliferation; cellular differentiation; cellular adhesion;  
 von Willebrand factor-associated disorder; cell trafficking; cancer;  
 hematoepithelial disease; atelectasis; pulmonary congestion;  
 oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;  
 intestinal disorder; spleen associated disease; renal disorder;  
 cardiovascular disorder; ischemic heart disease; hydrocephalus;  
 brain herniation; iatrogenic disease; inflammation; meningitis;  
 Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;  
 multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 6..764  
 FT /tag= a  
 FT /product= "TANGO 261"

FT sig\_peptide 6..89  
 FT /tag= b  
 FT mat\_peptide 90..764  
 FT /tag= c

XX WO200052022-A1.

XX 08-SEP-2000.

XX

PF 01-MAR-2000; 2000MO-US005226.  
 XX  
 PR 01-MAR-1999; 99US-0122458P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Barnes TM, Holtzman DA, Sharp JD, Fraser CJ;  
 XX  
 DR WPI; 2000-579269/54.  
 XX P-PSDS; AAB18449.  
 XX  
 PT Novel human and murine secreted proteins designated TANGO 216, 261, 262,  
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for  
 PT treating cancer.  
 XX  
 PS  
 XX Claim 2; Fig 5; 175pp, English.

The present sequence encodes a human TANGO 261 polypeptide. The  
 specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO  
 267. The TANGO polypeptides can be used to modulate cellular  
 proliferation, modulate cellular differentiation and/or modulate cellular  
 adhesion. The proteins can be used to treat any von Willebrand factor-  
 associated disorder, regulate extracellular matrix structuring, cellular  
 adhesion, and cell trafficking and/or migration, modulate cellular  
 interactions, modulate cell adhesion in proliferative disorders, such as  
 cancer, modulate the proliferation, differentiation, and/or function of  
 cells that appear in the bone marrow, and leukocytes, treat bone marrow,  
 blood and hematopoietic associated diseases and disorders, atelectasis,  
 pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial  
 asthma and bronchiectasis, intestinal disorders, spleen associated  
 diseases, modulate renal disorders, treat cardiovascular disorders such  
 as ischemic heart disease, modulate the proliferation, differentiation,  
 and/or function of bone and cartilage cells and to treat bone and/or  
 cartilage associated diseases or disorder. They may also be used to treat  
 disorders associated with the ovaries, cerebral oedema, hydrocephalus,  
 brain herniations, iatrogenic disease, inflammations, bacterial and viral  
 meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's  
 disease, multiple sclerosis, brain cancers, hydrocephalus and  
 encephalitis, and treat hepatic disorders

Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;

Query Match 60.8%; Score 803.2; DB 3; Length 969;  
 Best Local Similarity 99.6%; Pred. No. 4.3e-117;  
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 514 GGAATCAACGAGCTGAGTTGTTCAATCATCATCATCTGTGTGATGATGAT 573  
 Db 2 GGAATGAGCGAGAGCTGAGTTGTTCAATCATCATCATCTGTGTGATGATGAT 61  
 QY 574 GGTGTGTATATACGTGCTGAGCACTAACAAGTGTGTGATGATGATGAT 633  
 Db 62 GGTGTGTATATACGTGCTGAGCACTAACAAGTGTGTGATGATGATGAT 121  
 QY 634 CCGGACAGCGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693  
 Db 122 CCGGACAGCGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181  
 QY 694 CTCGAGAGCAAGTGTGAGCAAGAGATCCAGAGCCGAGGTTACGCGCGCTCG 753  
 Db 182 CTCGAGAGCAAGTGTGAGCAAGAGATCCAGAGCCGAGGTTACGCGCGCTCG 241  
 QY 754 GCCACCGAGCGCTGCGCGCTGCGCGCTTGGCCAGCGGAGGCTTCCACCGCTTCCA 813  
 Db 242 GCCACCGAGCGCTGCGCGCTGCGCGCTTGGCCAGCGGAGGCTTCCACCGCTTCCA 301  
 QY 814 GCCACCGATCTGATACGTGAGCAAGAGATGACCTGAGCAACCATCTGCTGTGAGA 873  
 Db 302 GCCACCGATCTGATACGTGAGCAAGAGATGACCTGAGCAACCATCTGCTGTGAGA 361  
 QY 874 CCGGAGAGAGCGCCCACTTCAAGAGGCGCTGAGCACTTCAAGGTTGGAGACCCGAGCA 933  
 Db 362 CCGGAGAGAGCGCCCACTTCAAGAGGCGCTTCAAGGTTGGAGACCCGAGCA 421



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OY 934 GAGCTGGAACCTGAACCGGGAGTCGGTGGCCGACACCCCAACAGAACCATCTTGACAG 993
DB 422 GAGCTGGAACCTGAACCGGGAGTCGGTGGCCGACACCCCAACAGAACCATCTTGACAG 481
OY 994 TGACCTGATGATAGTGGCCAGGCTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGGCAT 1053
DB 482 TGACCTGATGATAGTGGCCAGGCTGGGCGGCCCCCTGCCCCCAGCAGTAACTCGGGCAT 541
OY 1054 CAGCGCCACGTGCTACGGCAGCGCGCGGGCGCATGGAAGGGGCGCGCCGCCACTACAGCGA 1113
DB 542 CAGCGCCACGTGCTACGGCAGCGCGGGCGCATGGAAGGGGCGCGCCGCCACTACAGCGA 601
OY 1114 GGTCAATCGGCCACTACCGGGGTCCTCTCTTCCAGCACACGACAGAGAGTGGGCGGCTTC 1173
DB 602 GGTCAATCGGCCACTACCGGGGTCCTCTCTTCCAGCACACGACAGAGAGTGGGCGGCTTC 661
OY 1174 CTGGCTGAGGGGAGCCCGGCTCCACCAACACATCGGCGCCCTAGAGAGCGCAGCCAT 1233
DB 662 CTGGCTGAGGGGAGCCCGGCTCCACCAACACATCGGCGCCCTAGAGAGCGCAGCCAT 721
OY 1234 CTGAGCAAGAAGAGATTAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCCG 1293
DB 722 CTGAGCAAGAAGAGATTAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCCG 781
OY 1294 GGCTGGGGCTGCGTAGGTGAAAAAGGCG 1321
DB 782 GGCTGGGGCTGCGTAGGTGAAAAAGGCG 809
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-934-249-1

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Scoring table: IDENTITY NUC  
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Searched: 41078325 seqs, 23393541228 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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EST:  
1: gb\_est1:  
2: gb\_est2:  
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4: gb\_hic:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_g881:  
10: gb\_g882:  
11: gb\_g883:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	859.4	65.1	1005	1	AL578575
C 2	858.8	65.0	1038	1	AL571750
3	766.8	58.0	967	5	BQ641849
4	766	58.0	1046	3	BM922276
5	764.2	57.9	1059	1	AL543170
6	741	56.1	901	4	CR612083
7	736.4	55.6	916	5	BQ954555
C 8	734.2	55.7	850	1	AL558881
C 9	715	54.1	867	5	BX362396
10	714.6	54.1	897	1	AL558882
11	691.2	52.3	945	5	BUS39219
12	686.6	52.0	850	5	BUS39219
13	651	49.3	780	10	AY419334
14	637.4	48.3	647	8	AY419334
15	634.2	48.0	711	7	CJ028468
16	630.6	47.7	1207	4	AK008976
17	614.6	46.5	782	3	BQ015170
C 18	607.4	46.0	609	5	BQ636742
19	591.4	44.6	601	8	DN991959
20	588.8	44.6	605	7	CV028567
21	578.4	43.8	890	5	BQ690750
22	570.4	43.2	973	5	BU169156

C 23	568.8	43.1	572	5	BX641317	BX641317 DKFZp686K
C 24	567.4	43.0	729	5	BQ575741	BQ575741 UI-H-E01-
C 25	564.8	42.8	730	5	BM677602	BM677602 UI-H-E01-
C 26	563.2	42.6	728	5	BQ683523	BQ683523 UI-CF-EC1
27	550	41.6	551	3	BM141979	BM141979 tE2sa1.Y
28	545	41.3	553	8	DN990606	DN990606 TC121025
29	529.8	40.1	894	3	BI851941	BI851941 603379004
30	521	39.4	1068	5	BUS27705	BUS27705 AGENCOURT
31	507	38.4	780	10	AY419335	AY419335 Pan trogl
C 32	501.6	38.0	588	3	BM483503	BM483503 536869 MA
C 33	493.6	37.4	693	1	AT761441	AT761441 w95f07.x
C 34	493.4	37.4	655	5	BQ691705	BQ691705 AGENCOURT
35	487.6	36.9	646	10	CG784226	CG784226 PHCRG-GT
36	486	36.8	1400	3	BM559329	BM559329 AGENCOURT
37	480.8	36.4	964	5	BUS59860	BUS59860 AGENCOURT
38	477.6	36.2	646	5	BUS59841	BUS59841 AGENCOURT
39	476.4	36.1	651	6	CB554226	CB554226 MMSPO052
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#### ALIGNMENTS

RESULT 1  
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DEFINITION AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
LOCUS CDNA clone CSODK001YC24 3-PRIME, mRNA sequence.

ACCESSION AL578575 GI:46257448  
VERSION AL578575.3  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1005)  
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
TITLES Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 16, 2001 this sequence version replaced gi:31316780.

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9945.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdnas=CSODK001B12NP1LC=9945.r.  
Location/Qualifiers

#### FEATURES

source

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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

[illegible]

ACCESSION	CS00DA008YB23 3--PRIME, mRNA sequence.
VERSION	AL517150
KEYWORDS	AL517150.3 GI:45653717
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL	Hominidae; Homo.
COMMENT	1 (bases 1 to 1038) L1,W.B., Gruber,C., Jessee,J. and Polyes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 13, 2001 this sequence version replaced gi:30492472. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna/s=CS00DA008CA12NP1&c=945.r.

FEATURES	source
Location/Qualifiers	1..1038
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="CSODA008YB23"
	/tissue_type="NEUROBLASTOMA"
	/clone_lib="Homo sapiens NEUROBLASTOMA"
	/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

Query Match	Best Local Similarity	Matches	95.0% ; Score 858.8 ; DB 1 ;	96.4% ; Pred. No. 1.1e-149 ;	7 ; Mismatches 24 ;	Indels 2 ;	Gaps 2 ;
QY	398	GCCTGCGCGCGCGCTGCATGACGACCGGCTTGATGAGGGGTCAACAGACACCGCGCGCGCGCGCC	457	1038	GCCTGCGCGCGCGCTGCATGACCGCGCTTGATGAGGGGTCAACAGACACCGCGCGCGCC	980	
QY	458	GGGCGAGCCCAATGTCCTCTGACAGTGCACCTGCAAAAGCGCTTGTTCGAAGATGAG	517	979	GGGCGAGCCCAATTTCTCTGACAGTGCACCTGCAAAAGCTTTTGTTCGAAGATGAG	920	
QY	518	ATCAGGAGCTGAGATTGTTCAGATCATCATCATCTGCTGATGATGATGATGATG	577	919	ATCAGGAGCTGAGATTGTTCAGATCATCATCATCTGCTGATGATGATGATGATG	860	
QY	578	GTGTGATCATGCTGCTCTGAGGCCATCAAGCTGTCTGCACGCTCTTATCAGCCGG	637	859	GTGTGATCATGCTGCTCTGAGGCCATCAAGCTGTCTGCACGCTCTTATCAGCCGG	800	
QY	638	CACAGCCAGGGGGCGGAGAGAGATGCTCCTGTCTCTCAGAAAGATGCTGTGCGCTCG	697	759	CACAGCCAGGGGGCGGAGAGAGATGCTCCTGTCTCTCAGAAAGATGCTGTGCGCTCG	740	
QY	698	GAGAGCAGTGTCTAGCGCAACGGAATCCCAAGCGCGCAGGTCTACGCGCGCTTGCGCC	757	729	GAGAGCAGTGTCTAGCGCAACGGAATCCCAAGCGCGCA-GTCTACGCGCGCGCTTGCGCC	681	
QY	758	ACCGACCGCTTGCGCTGCGCGCGCTTGCGCGCGGAGGCGGCTTCACGCTTCAGCGCC	817	680	ACCGACCGCTTGCGCTGCGCGCGCTTGCGCGCGGAGGCGGCTTCACGCTTCAGCGCC	621	



	ACCESSION	BW922276
	VERSION	BW922276.1
	KEYWORDS	EST.
	SOURCE	GI:19372655
	ORGANISM	Homo sapiens (human)
		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
		Hominidae; Homo.
	REFERENCE	1 (bases 1 to 1046)
	AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
	JOURNAL	Unpublished (1999)
	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLM12791 row: n column: 06 High quality sequence stop: 671. Location/Qualifiers
FEATURES	source	1..1046 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5754437" /lab_host="DH10B" /clone_lib="NIH_MGC_115" /note="Torgan: pooled brain, lung, testis; Vector: pCMV-Sport8; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."
ORIGIN		
Query Match	58.0%; Score 766; DB 3; Length 1046;	
Best Local Similarity	95.8%; Pred. No. 2.1e-132;	
Matches 818; Conservative	0; Mismatches 32; Indels 4; Gaps 3	
Db	347 CGGCGGGAGCCGCCCGGGCGCCCGGAGCCCCCGGGCGCCGCGCGCCGCGC	406
	1 CGGGCGGGAGCCCCCCCCCGGGCGCCCGGAGCCCCCGGGCGCCGCGCGCCGCGC	60
Db	407 CCGTCATAGCAACCGCTTGATGGGGGTCAACAAGACCAGCCGCGCGCGCGGACGCC	466
	61 CGGTCAATGCAACCGCTGATTGGGGGTCAACAAGACCAGCCGCGCGCGCGGACGCC	120
Db	467 AATGTTCTCTGCACGTGCACATGCAAAACGCTCTTTGTTCAAGCATGGAATCACGGAG	526
	121 AATGTTCTCTGCACGTGCACATGCAAAACGCTCTTTGTTCAAGCATGGAATCACGGAG	180
Db	527 CTGGAGTTTGTTCAGATCATCATCATCGTGTTGGTGGATGATGGTGGTGGATGATC	586
	181 CTGGAGTTTGTTCAGATCATCATCATCGTGTTGGTGGATGATGGTGGTGGATGATC	240
Db	587 ACSTGCTCTGAGCCACTACAAAGCTGTCTGCACGGTCTCTTATCAGCCGCGGACAGCCAG	646
	241 AGCTGCTCTGAGCCACTACAAAGCTGTCTGCACGGTCTCTTATCAGCCGCGGACAGCCAG	300
Db	647 GGGCGGAGAGAAGAAATGCCCTGTTCTCAAGAAAGATGCTGTGTGCGCTTGGAGAGACACA	706
	301 GGGCGGAGAGAAGAAATGCCCTGTTCTCAAGAAAGATGCTGTGTGCGCTTGGAGAGACACA	360
Db	707 GTGTCAAGGCAAGGAATCCCAAGCCGCGAGGTTAAGCCCCGCTCGGCGCCACCAACCGCG	766

Db	361	GTGTCAAGGCAACGAAATCCAGAGCCGACAGTCTACGGCCCGCCTCGGCCACCGACCGC	420
Qy	767	CTGGCCGTGTGCGCCCTTTCGCCACAGCGGAGCGTCTTCAACGCTTTCAGAGCCACCTATACG	826
Db	421	CTGGCCGTGTGCGCCCTTTCGCCACAGCGGAGCGTCTTCAACGCTTTCAGAGCCACCTATACG	480
Qy	827	TACCTGCAGACAGATCGACTGSCACCCACCATCTCGCTGTTCAGACGGGAGAGAGCC	886
Db	481	TACCTGCAGACAGATCGACTGSCACCCACCATCTCGCTGTTCAGACGGGAGAGAGCC	540
Qy	887	CCACCCCTACAGAGGCGCCCTTGACCTTCAGCTTCGGGACCCCGAGACGACGTGAACTG	946
Db	541	CCACCCCTACAGAGGCGCCCTTGACCTTCAGCTTCGGGACCCCGAGACGACGTGAACTG	600
Qy	947	AACCGGAGATCGCTGTCGCCGACACCCCAAAGAACCATCTTTCGACAGTGAACCTGATGAT	1006
Db	601	AACCGGAGATCGCTGTCGCCGACACCCCAAAGAACCATCTTTCGACAGTGAACCTGATGAT	660
Qy	1007	AGTGCAGAGGTGGGGCGCGCCCTGCGCCCGACAGCATTAACCTCGGACATCAGCGCACCTGC	1066
Db	661	AGTGCAGAGGTGGGGCGCGCCCTGCGCCCGACAGCATTAACCTCGGACATCAGCGCACCTGC	720
Qy	1067	TACGGCAGCGCGCGG-GCGCATGTGAGGAGGCGCGCG-CCACCTACAGCGAGTCACTGAGCC	1124
Db	721	TACGGCAGCGCGCGCGCGCATGTGAGGAGGCGCGCGCCCACTACAGGAGGTCACTGAGCC	780
Qy	1125	ACTA--CCCGGGGTCTCTCTTCCAGACACAGACAGAGATGGGGCGCCCTCTCTTGTCTGA	1182
Db	781	ACTAATCCCGGGGGGTCTCTCTTCCAGACACANCATACACTGGGGCGCGCCCTCTCTTGC	840
Qy	1183	GGGGACCGCGGCTCC 1196	
Db	841	CTGGAGAGGGAGCC 854	
RESULT 5			
AL543170			
LOCUS	AL543170	1059 bp	mRNA linear EST 24-MAR-2004
DEFINITION	AL543170 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA		
VERSION	clone CSOD1002Y103 5-PRIME, mRNA sequence.		
ACCESSION	AL543170		
KEYWORDS	AL543170.3 GI:45718734		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
JOURNAL	Hominidae; Homo.		
COMMENT	1 (bases 1 to 1059)		
	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.		
	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	On Feb 15, 2001 this sequence version replaced gi:31265017.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
	Email: beqre@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	1st strand cDNA was primed with a NotI-Oligo (dT) primer. Five primers		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by life Technologies, a		
	division of Invitrogen. This sequence belongs to sequence cluster		
	9945.r		
	For more information about this cluster, see		
	http://www.genoscope.cns.fr/cdna?c=CSOD1002AB02QP1&c=9945.r.		
FEATURES	Location/Qualifiers		
source	1..1059		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CSOD1002Y103"		
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## ORIGIN

/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 57.9%; Score 764.2; DB 1; Length 1059;  
 Best Local Similarity 91.1%; Pred. No. 4.5e-132;  
 - Matches 866; Conservative 20; Mismatches 54; Indels 11; Gaps 7;

102 GCGGAGAGGCTCACCCCGGCGAGCGCGCCCTGCGACGCCATTTTCGAGAG 161  
 1 GCGGAGAGGCTCACCCCGGCGAGCGCGCCCTGCGACGCCATTTTCGAGAG 60  
 162 CCACCCCGGCGAGCTGCGAGCGCCCGGCGCTGCGAGGAGCGCGGCGGCGAGC 221  
 61 CCACCCCGGCGAGCTGCGAGCGCCCGGCGCTGCGAGGAGCGCGGCGGCGAGC 120  
 222 GAGAGCGGCTGCGCGAGCTGAGCGCCCGGCGCGCCCGGGAATTGGGCGGAGCCGAGC 281  
 121 GACGCGCGGCTGCGCGAGCTGAGCGCCCGGCGCGCCCGGGAATTGGGCGGAGC 180  
 282 CCGGCGAGCGGCGCGCGCTGCGCGCGCGCGCGCTGCGATGCGGCGCGCGAGCTC 340  
 161 CCGGCGAGCGGCGCGCGCTGCGCGCGCGCGCGCTGCGATGCGGCGCGCGAGCTC 240  
 341 CCGGCGCGGCGCGAGCGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 400  
 241 CCGGCGCGGCGCGAGCGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 300  
 401 GCGGCGCGGCTGCGATGAGCGGCTGAGCGAGCGCGCGCGCGCGCGCGCGCGCGC 460  
 301 GCGTACCTTTTCATGACCGCTTTTATGGGCTTACAGAGCGCGCGCGCTTCCCTGC 360  
 461 CAGCCCAATGTCCTCGAC--GTGCACTGCAAGAGCTTGTTCAGAGCATGAGA 518  
 361 WACCCCAATTTCTTCTTCACTTGTTCATTTCAACACTTTTTCATTAACATGAGA 420  
 519 TCACGAGCTGAGTTTGTTCATGATCATGATGATGATGATGATGATGATGATGATG 578  
 421 TCACGAGCTGAGTTTGTTCATGATCATGATGATGATGATGATGATGATGATGATG 480  
 579 TGGTATCATGTCGCTGCGAGCGCACTAGAGTGTGTGCAAGGCTTTCATCAGCGCGC 638  
 481 TGGTATCATGTCGCTTGTGAGCGCACTAGAGTGTGTGCAAGGCTTTCATCAGCGCGC 540  
 639 ACAGCGAGGCGGAGAGAGAGATGCCCTGCTCAGAGAGATGCCCTGCGCGCTGCG 698  
 541 ACAGCGAGGCGGAGAGAGAGATGCCCTGCTCAGAGAGATGCCCTGCGCGCTGCG 600  
 699 ACAGCGAGTGTGAGCAAGAGATGCCAGAGCGCGAGCTTACGCCCGCTGCGCGCA 758  
 601 ACAGCGAGTGTGAGCAAGAGATGCCAGAGCGCGAGCTTACGCCCGCTGCGCGCA 660  
 759 CCGAGCGCTGCGCGCTGCGCGCTTGTGCGAGCGGAGCGCTTTCACCGCTTTCAGCCA 818  
 661 CCGAGCGCTGCGCGCTGCGCGCTTGTGCGAGCGGAGCGCTTTCACCGCTTTCAGCCA 720  
 819 CCTATCCGTAACCTGAGAGAGATGAGCTGCAACCAACATGCTGCTGAGAGCGGAG 878  
 721 CCTATCCGTAACCTGAGAGAGATGAGCTGCAACCAACATGCTGCTGAGAGCGGAG 780  
 879 AGGAGCGCCCACTTACAGAGCGCCCTGCAACCTTCCAGCTTTCGAGAGCGAGCAGC 938  
 781 AGGAG--CCCACTTACAGAGCGCCCTGCAACCTTCCAGCTTTCGAGAGCGAGCAGC 837  
 939 TGGAGCTGAACTGAGAGTGTGCGCGAGCGCCCAACAGAGACATCTTTCAGAGAGAGC 998  
 838 TGGAGCTGAACTGAGAGTGTGCGCGAGCGCCCAACAGAGACATCTTTCAGAGAGAGC 895  
 999 TGAATGATAGTGCAGGCTGCGGAGCGCCCGCGCGAGCAGTAACTGCG 1049  
 896 TGAATGATAGTGCAGGCTGCGGAGCGCCCGCGCGAGCAGTAACTGCG 943

## RESULT 6

CR612083

## LOCUS

CR612083 901 bp mRNA linear HTC 21-JUL-2004

## DEFINITION

Full-length cDNA clone CS0D015F12 of T cells (Jurkat cell line)

## ACCESSION

CR612083

## VERSION

CR612083.1

## KEYWORDS

HTC; CNSLT\_CDNA.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 901)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Parade Avenue

2 (bases 1 to 901)

Genoscope.

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)

- Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen

Location/Qualifiers

1..901

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D015F12"

/tissue\_type="T cells (Jurkat cell line) Cot

10-normalized"

/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 56.1%; Score 741; DB 4; Length 901;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-128;  
 - Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

581 GTGATCAGTGTGCTGAGCGCACTAGAGTGTGTGCAAGGCTTCTCATCAGCGCGCAG 640  
 1 GTGATCAGTGTGCTGAGCGCACTAGAGTGTGTGCAAGGCTTCTCATCAGCGCGCAG 60  
 641 AGCCAGGGGCGGAGAGAGAGATGCCCTGCTCAGAGAGATGCTGTGCGCTTCGAG 700  
 61 AGCCAGGGGCGGAGAGAGATGCCCTGCTCAGAGAGATGCTGTGCGCTTCGAG 120  
 701 AGCAGAGTGTGAGCAAGAGATGCCAGAGCGCGAGCTTACGCCCGCTGCGCGCAC 760  
 121 AGCAGAGTGTGAGCAAGAGATGCCAGAGCGCGAGCTTACGCCCGCTGCGCGCAC 180  
 761 GACCGCTGCGCGCTGCGCGCTTGTGCGAGCGGAGCGCTTCAACCGCTTTCAGGCCAC 820  
 181 GACCGCTGCGCGCTGCGCGCTTGTGCGAGCGGAGCGCTTCAACCGCTTTCAGGCCAC 240  
 821 TATCGTACTGTCAGAGAGATGAGCTGCGAGCCCAACCATCTGCTGTCAGAGCGGAG 880  
 241 TATCGTACTGTCAGAGAGATGAGCTGCGAGCCCAACCATCTGCTGTCAGAGCGGAG 300  
 881 GAGCCCGCACTTACAGAGCGCCCTGCGAGCGCTTTCAGAGCTTTCGAGAGAGAGC 940  
 301 GAGCCCGCACTTACAGAGCGCCCTGCGAGCGCTTTCAGAGCTTTCGAGAGAGAGC 360  
 941 GAACTGAACTGAGAGTGTGCGCGAGCGCCCAACAGAGACATCTTTCAGAGAGAGC 1000



Db 361 GAACTGAACCGGAGATCGGTGGCGGACCCCAACAGACCATTTTGACAGTACCTG 420  
Qy 1001 ATGATAGTCCAGGCTGAGCGGCGCCCTGCCCCCAGACAGTACTCGGACATACGCC 1060  
Db 421 ATGATAGTCCAGGCTGAGCGGCGCCCTGCCCCCAGACAGTACTCGGACATACGCC 480  
Qy 1061 ACGTCTACGCGAGCGGCGGCGGCGATGAGAGGCGCGCCCACTAGAGAGGTCAATC 1120  
Db 481 ACGTCTACGCGAGCGGCGGCGGCGATGAGAGGCGCGCCCACTAGAGAGGTCAATC 540  
Qy 1121 GGCCTACACCGGAGGCTCTCTTCCAGACACGACAGAGTGGCGCCCTCTTGGCTG 1180  
Db 541 GGCCTACACCGGAGGCTCTCTTCCAGACACGACAGAGTGGCGCCCTCTTGGCTG 600  
Qy 1181 GAGGAGACCGGCTCCACCAACACATCGCGCCCTTAGAGAGCGACCATCTGAGC 1240  
Db 601 GAGGAGACCGGCTCCACCAACACATCGCGCCCTTAGAGAGCGACCATCTGAGC 660  
Qy 1241 AAAGAGAGATTAACAGAAAGACACCTCTCTAGGCTCCCAAGGGGGCGGGCTGG 1300  
Db 661 AAAGAGAGATTAACAGAAAGACACCTCTCTAGGCTCCCAAGGGGGCGGGCTGG 720  
Qy 1301 GCTGCTAGGTGAAGGCGAG 1321  
Db 721 GCTGCTAGGTGAAGGCGAG 741

RESULT 7  
B0954555 916 bp mRNA linear EST 21-AUG-2002  
LOCUS B0954555  
DEFINITION IMAGE:6204609 5', mRNA sequence.

ACCESSION B0954555  
VERSION B0954555.1 GI:22370033  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 916)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: L1AM13626 row: C column: 10  
High quality sequence stop: 669.  
Location/Qualifiers

## FEATURES

source

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6204609"  
/sex="male"  
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/dev\_stage="adult, 70 yr"  
/lab\_host="DH10B"  
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/note="Vector: PCW-Sports (Life Technologies); Site\_1:  
NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCAGCGTCCG-3' and  
5'-GACTAGTCTAGATCGGCGGCGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.87 kb. This is a primary

## ORIGIN

Query Match 55.7%; Score 736.4; DB 5; Length 916;  
Best Local Similarity 95.7%; Pred. No. 6.8e-127;  
Matches 800; Conservative 0; Mismatches 31; Indels 5; Gaps 4;

Library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

Qy 344 GCGCGGCGGAGGCCCCCGCGCGCCCGAGCCCCCGCGCGCGCGCGCGCC 403  
Db 1 GCGCGGCGGAGGCCCCCGCGCGCCCGAGCCCCCGCGCGCGCGCGCGCC 60  
Qy 404 GCGCGGCGGAGGCCCCCGCGCGCCCGAGCCCCCGCGCGCGCGCGCGCC 463  
Db 61 GCGCGGCGGAGGCCCCCGCGCGCCCGAGCCCCCGCGCGCGCGCGCGCC 120  
Qy 464 CCCAATGCTCTCTCAGTGAAGCTGCTTTGTTCCAGACATGAGATGACG 523  
Db 121 CCCAATGCTCTCTCAGTGAAGCTGCTTTGTTCCAGACATGAGATGACG 180  
Qy 524 GAGCTGAGATTGTTCAATCATCATCATGCTGCTGATGATGATGATGATG 583  
Db 181 GAGCTGAGATTGTTCAATCATCATCATGCTGCTGATGATGATGATGATG 240  
Qy 584 ATCACTGCTCTCTGAGGCTTACAGCTGCTGCTGCTGCTGCTGCTGCTG 643  
Db 241 ATCACTGCTCTCTGAGGCTTACAGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Qy 644 CAGGCGGAG 703  
Db 301 CAGGCGGAG 360  
Qy 704 ACAGTGTGAGGCAACGAGATCCAGAGCGGAGCTTACAGCGCTTCCAGCCAT 763  
Db 361 ACAGTGTGAGGCAACGAGATCCAGAGCGGAGCTTACAGCGCTTCCAGCCAT 420  
Qy 764 GCGCTGCGGCTGCGCGCTTCCAGAGGAGGCTTCCAGCGCTTCCAGCCAT 823  
Db 421 GCGCTGCGGCTGCGCGCTTCCAGAGGAGGCTTCCAGCGCTTCCAGCCAT 480  
Qy 824 CCGTACTGAGAGAGAGATGAGCTGCAACCCACATCTGCTGAGAGAGAGAG 883  
Db 481 CCGTACTGAGAGAGATGAGCTGCAACCCACATCTGCTGAGAGAGAGAG 540  
Qy 884 CCCCACCTTACAGAGGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAG 943  
Db 541 CCCCACCTTACAGAGGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAG 600  
Qy 944 CTGAACCGGAGTGGTGGCGGACCCCAAGAACATCTTCCAGAGTGAATG 1003  
Db 601 CTGAACCGGAGTGGTGGCGGACCCCAAGAACATCTTCCAGAGTGAATG 660  
Qy 1004 GATAGTGC-AGGCTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1061  
Db 661 GATAGTGC-AGGCTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
Qy 1062 CGTGTACGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1120  
Db 721 CGTGTACGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
Qy 1121 GAGCA-CTACCGGCGGCTCTCTTCCAGACACGACAGAGAGAGAGAGAG 1174  
Db 781 GAGCACTACCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836

RESULT 8  
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LOCUS AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
DEFINITION Homo sapiens cDNA clone CS0D015VF12 3-PRIME, mRNA sequence.  
ACCESSION AL558881

VERSION AL558881.3 GI:46184268  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo  
 1 (bases 1 to 850)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31283014.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 9945.x  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?c=CS0D015DC06NP1&c=9945.r.  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D015YR12"  
 /cell\_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
 /clone\_1ib="Homo sapiens T CELLS (JURKAT CELL LINE) COT  
 10-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and Ecor V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 55.6%; Score 734.2; DB 1; Length 850;  
 Best Local Similarity 99.3%; Pred. No. 1.8e-126;  
 Matches 736; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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 850 GTGATCAGCTGCTGCTGAGCCACTACAGCTGTGTGACGGTCTTATCATCGCGGAC 791  
 |||||  
 641 AGCCAGGGGCGGAGAGAGAGATGCTCTCTCAAGAGATGCTGTGGCCCTTCGGAG 700  
 |||||  
 790 AGCCAGGGGCGGAGAGAGATGCTCTCTCTCAAGAGATGCTGTGGCCCTTCGGAG 731  
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 701 AGCAGAGTGTGAGGAGAGAGATGCTCTCTCTCAAGAGATGCTGTGGCCCTTCGGAG 760  
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 730 AGCAGAGTGTGAGGAGAGAGATGCTCTCTCTCTCAAGAGATGCTGTGGCCCTTCGGAG 671  
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 761 GACCGCTGCGCGCTGCT 820  
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 670 GACCGCTGCGCGCTGCT 611  
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 821 TATCGCTGCTGAGAGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 880  
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 610 TATCGCTGCTGAGAGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 551  
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 881 GAGCCCGCCCTTACAGAGGCGCCCTGACCTTCAGCTTCGAGAGAGAGAGAGAGAGAG 940  
 |||||  
 550 GAGCCCGCCCTTACAGAGGCGCCCTGACCTTCAGCTTCGAGAGAGAGAGAGAGAGAG 491  
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 941 GAAGTGAACCGGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1000  
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 490 GAAGTGAACCGGAGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431  
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 1001 ATGAGATAGTGCAGAGCTGGGGGCGCCCTGCGCCCGCCAGAGAGATCTGGGGCATCGAGCC 1060

Db 430 ATGAGATAGTGCAGAGCTGGGGGCGCCCTGCGCCCGCCAGAGATCTGGGGCATCGAGCC 371  
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 Qy 1061 AGCTGTACAGGACAGCGCGCGCGCGCATGTGAGAGGCGCGCGCCACTTACAGAGAGTATC 1120  
 |||||  
 Db 370 ACCTGTACAGGACAGCGCGCGCGCATGTGAGAGGCGCGCGCCACTTACAGAGAGTATC 311  
 |||||  
 Qy 1121 GGCCTACAGCGCGCGCGCGCGCATGTGAGAGGCGCGCGCCACTTACAGAGAGTATC 1180  
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 Db 310 GGCCTACAGCGCGCGCGCGCGCATGTGAGAGGCGCGCGCCACTTACAGAGAGTATC 251  
 |||||  
 Qy 1181 GAGGAGAGCGCGCGCTCCACACACACATGCGCGCGCTTACAGAGAGAGAGAGAGAGAG 1240  
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 Db 250 GAGGAGAGCGCGCGCTCCACACACACATGCGCGCGCTTACAGAGAGAGAGAGAGAGAG 191  
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 Qy 1241 AAGAGAGAGTAAACAG 1300  
 |||||  
 Db 190 AAGAGAGAGTAAACAG 131  
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 Qy 1301 GCTGCTAGTGTGAAGAGAGAG 1321  
 |||||  
 Db 130 GCTGCTAGTGTGAAGAGAGAG 110  
 |||||

RESULT 9  
 BX362396/c 867 bp mRNA linear EST 08-APR-2004  
 LOCUS BX362396 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
 DEFINITION Homo sapiens cDNA clone CS0D014YN15 3-PRIME, mRNA sequence.  
 ACCESSION BX362396  
 VERSION BX362396.2 GI:46307643  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 867)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 5, 2003 this sequence version replaced gi:30378625.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 9945.x  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?c=CS0D014CG08NP1&c=9945.r.  
 FEATURES  
 source  
 1..867  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D014YN15"  
 /cell\_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
 /clone\_1ib="Homo sapiens T CELLS (JURKAT CELL LINE) COT  
 10-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and Ecor V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 54.1%; Score 715; DB 5; Length 867;  
 Best Local Similarity 96.2%; Pred. No. 6.5e-123;  
 Matches 731; Conservative 16; Mismatches 11; Indels 2; Gaps 2;

OY		563	ATATGAGTGAATGGAGTGATGATC-ACCTGCTGTGAGCCACTACAAGCTGTGCACG	621
Db		867	ATGATGTGTAATSGTGTGTSBTATCTMCTGCTCTGTGACCATTACAGCTGTCTGCACG	808
OY		622	GTCCTTCAATCACCGGCCACAGCCCAAGGGCGAGAGAGAAGATGCTCTGTCTCAANAAG	681
Db		807	GTCCTTCAATCAGCCSBCACACGACGAGGGCGGAGAGAGMAATGCTCTKTYCTCAGAAGG	748
OY		682	ATGCTCTGTGGCCCTTCGAGAGACACAGTTCAAGGCAAACGGAAATCCCAAGCCGCAAGTCTA	741
Db		747	ATGCTYTKTGCGCYTCOGAAGACAAGTGTCAAGCAACGAAATCCCAAGCCGCA- GITYTA	689
OY		742	CGCCCCGCTCGAGCCCAACGACCGGCTGAGCGTGCAGCCCTTTCGCGCAAGCGAGCGCTT	801
Db		688	CGCCCCGCTTGGGCCCAACCGAACCGCTGTGGCCGTGCGCCCTTTCGCGCAAGCGAGCGCTT	629
OY		802	CCACCGCTTCAGCCCACTTATCCGTACCTGACAGACAGATGACCTTGCCAACCCACAT	861
Db		628	CCACCGCTTCAGCCCACTTATCCGTACNTGAGNAAGATGACNTGCGGCCACCAT	569
OY		862	CTCGCTGTCAACGGGGAGAGAGCCCCCAACCTTACAGAGGCCCTTGCAACCTTCAGCTTG	921
Db		568	CTCGCTGTCAACGGGGAGAGAGCCCCCAACCTTACAGAGGCCCTTGCAACCTTMA GTTTCG	509
OY		922	GGA CCCCAGAGCGAGCTGGAACTGAACCGGGAGTCCGCTGCGCGCAACCCCCAAGAAAC	981
Db		508	GGA CCCCAGAGAGCGAGCTGGAACTGAACCGGGAGTCCGCTGCGCGCAACCCCCAAGAAAC	449
OY		982	CATCTTCGACAGTGAACCTGATGATGATGTCAGAGCTGGAGCGAGCCCTTGCCCCCAGCAG	1041
Db		448	CATCTTCGACAGTGAACCTGATGATGATGTCAGAGCTGGAGCGAGCCCTTGCCCCCAGCAG	389
OY		1042	TAACTCGGGCATCAGCCGCCAGTGTCTTAGCGGACGCGCGGCGCATATGAGGGGCGCCGCG	1101
Db		388	TAACTCGGGCATCAGCCGCCAGTGTCTTAGCGGACGCGCGGCGCATATGAGGGGCGCCGCG	329
OY		1102	CACCTACAGCGAGGTCATCCGCGCACTAACCCGGGGTCTCTTTCAGACACAGCAGCAGCAG	1161
Db		328	CACCTACAGCGAGGTCATCCGCGCACTAACCCGGGGTCTCTTTCAGACACAGCAGCAGCAG	269
OY		1162	TGGGCGCGCCCTCTTGTGTGAGGGGACCGGCTCCACACACACATCGCGCCCTTAGA	1221
Db		268	TGGGCGCGCCCTCTTGTGTGAGGGGACCGGCTCCACACAMMACATCGCGCCCTTAGA	209
OY		1222	GAGCGCAGCCATCTGAGCAAAAGAGAAGATTAACAAGAAAGCAACCTCTTAGGGTTC	1281
Db		208	GAGCGCAGCCATCTGAGCAAAAGAGAAGATTAACAAGAAAGCAACCTCTTAGGGTTC	149
OY		1282	CGAGGGGGCGGGGCTTGGGGCTGCGCTAAGTGA AAAAGCAG 1321	
Db		148	CGAGGGGGCGGGGCTTGGGGCTGCGCTAAGTGA AAAAGCAG 109	

RESULT	10
AL558882	
LOCUS	897 bp mRNA linear EST 02-APR-2004
DEFINITION	AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
ACCESSION	Homo sapiens cDNA clone CSDDV01SF12.5-PRIME, mRNA sequence.
VERSION	AL558882
KEYWORDS	AL558882.3 GI:46184269
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL	Homnidae; Homo.
COMMENT	1 (bases 1 to 897)
	Li W.B., Gruber C., Jesse J. and Polayes D.
	Full-length cDNA libraries and normalization
	Unpublished (2001)
	On Feb 15, 2001 this sequence version replaced gi:31283015.
	Contact: Genoscope

Genoscope - Centre National de Séquençage  
2 rue Gaston Cremieux. CP 5706 - 91057 Evry cedex - FRANCE  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
The left strand cDNA was primed with a NotI-oligo (dT) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalised. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9945.r  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?ts=CS0DJ015DC06Qp1&c=9945.r>.  
Location/Qualifiers  
1. .897  
/locusid="Homo\_sapiens"

## ORIGIN

Query Match	54.1%	Score 714.6	DB 1	Length 897
Best Local Similarity	99.3%	Pred. No. 7.8e-123		
Matches 736	Conservative 2	Mismatches 1	Indels 2	Gaps 2

OY	581	GTGATATCAGTCCGCTCGATGAGCAGCTTACAAAGCTGTCTCAGCAGCTCTTCTATCAGTCCGAC	84
Db	1	GTGATATCAGTCCGCTCGATGAGCAGCTTACAAAGCTGTCTCAGCAGCTCTTCTATCAGTCCGAC	60
OY	641	AGCCAGGGGCGGAGAGAGAAATGTCCTGTCTCAGAAAGATGCTGTGGCCCTCGAG	700
Db	61	AGCCAGGGGCGGAGAGAGAAATGTCCTGTCTCAGAAAGATGCTGTGGCCCTCGAG	120
OY	701	AGCAGAGTGTACAGGCAACGGATCCCAAGCCGAGGTCTACGCCCCGCTCGGCCAC	760
Db	121	AGCAGAGTGTACAGGCAACGGATCCCAAGCCGAGGTCTACGCCCCGCTCGGCCAC	179
OY	761	GACCGCCTGGGCGCTGTCCGCTTTGGCCAGGGGAGGGCTTCGACCGCTTCGACCCAC	820
Db	180	GACCGCCTGGGCGCTGTCCGCTTTGGCCAGGGGAGGGCTTCGACCGCTTCGACCCAC	239
OY	821	TATCCGTATCTGACAGCAGATGACCTGTGCCACCAATCTGTGCTGTCAAGCGGGAG	880
Db	240	TATCCGTATCTGACAGCAGATGACCTGTGCCACCAATCTGTGCTGTCAAGCGGGAG	299
OY	881	GAGCCCCCAGCCTTACAGGGCCCCCTGTGCACCTTCAAGCTTGGGAAACCCGAGACAGACTG	940
Db	300	GAGCCCCCAGCCTTACAGGGCCCCCTGTGCACCTTCAAGCTTGGGAAACCCGAGACAGACTG	359
OY	941	GAACTGAAACCGGAGTGTGCTGCGGCAACCCCAAAAGAAACATCTTTCGACGTGACTG	1000
Db	360	GAACTGAAACCGGAGTGTGCTGCGGCAACCCCAAAAGAAACATCTTTCGACGTGACTG	419
OY	1001	ATGATATGTCGAGGCTGGGCTGGCCCCCTGTGCCCCCAGCACTAACTGGGCACTAAGGCC	1060
Db	420	ATGATATGTCGAGGCTGGGCTGGCCCCCTGTGCCCCCAGCACTAACTGGGCACTAAGGCC	479
OY	1061	ACGTGCTACGGCAGGCGGCGGCGCATGAGAGGGGCGCGCCCACTACAGGAGGTATC	1120
Db	480	ACGTGCTACGGCAGGCGGCGGCGCATGAGAGGGGCGCGCCCACTACAGGAGGTATC	539
OY	1121	GAGCACTACCGGGGGTCTCTCTTCAGACCCAGAGAGCACTGGGGCGGCTCTTGTCTG	1180
Db	540	GAGCACTACCGGGGGTCTCTCTTCAGACCCAGAGAGCACTGGGGCGGCTCTTGTCTG	599
OY	1181	GAGGGAGCCGGGCTTCACACACACATGGCGCCCTTAGAGAGCGGACGATCTGAGC	1240

	RESULT 11	
Bu	BUS39219	
	LOCUS	BUS39219
	DEFINITION	BUS39219 945 bp mRNA linear EST 13-SEP-2002
	ACCESSION	AGNCOURT_10215265 NIH MGC_107 Homo sapiens cDNA clone
	VERSION	IMAGE:6569922 5', mRNA sequence.
	KEYWORDS	BUS39219
	SOURCE	BUS39219.1 GI:22849660
	ORGANISM	EST.
		Homo sapiens (human)
		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
		Homnidae; Homo
	REFERENCE	1 (bases 1 to 945)
	AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
	JOURNAL	Unpublished (1999)
	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC
		cDNA Library Preparation: Rubin Laboratory
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
		DNA Sequencing by: Agencourt Bioscience Corporation
		Clone distribution: MGC clone distribution information can be
		found through the I.M.A.G.E. Consortium/ILNL at:
		http://image.llnl.gov
		Plate: LLCM2757 row: p column: 18
		High quality sequence stop: 663.
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	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone IMAGE:6569922"	
	/tissue type="adenocarcinoma, cell_line"	
	/lab host="DH10B (phage-resistant)"	
	/clone_lib="NIH_MGC_107"	
	/note="Organ: breast; Vector: POTB7; Site 1: EcORI;	
	Site 2: XhoI; cDNA made by oligo-dT priming.	
	Directionally cloned into EcORI/XhoI sites using the	
	following 5' adaptor: GGCACGAG(G). Library constructed by	
	ling Hong in the laboratory of Gerald M. Rubin (University	
	of California, Berkeley) using ZAP-cDNA synthesis kit	
	(Stratagene) and Superscript II RT (Life Technologies).	
	Note: this is a NIH_MGC Library."	
ORIGIN		
Query Match	52.3%; Score 691.2; DB 5; Length 945;	
Best Local Similarity	93.7%; Pred. No. 1.8e-118;	
Matches 764; Conservative	0; Mismatches 44; Indels 7; Gaps 4;	
Bu		
Oy	499 TTGTTCGAGCATGATCAGCAAGCTGGAGTTTGTCAGATCATCATCATCGTGT	558
	65 TCTCTCGCAAACCAAGCAATGCCGAGCTGAGATTGTTCAGATCATCATCATGTGT	124
Bu		
Oy	559 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	618
	125 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	184
Oy	619 AAGGTCCTTCATCACGCCGACACAGCAAGGCGGAGAGAGAAGAAAGTGCCTGCTCA	678
Bu		
Oy	185 ACGGTCCTTCATCACGCCGACACAGCAAGGCGGAGAGAGAAGAAAGTGCCTGCTCA	244

QY	679	AGAGTACTGCTTGAGCCCTCTCGAGAGACACAGTGTATAGGCAACAGATATCCAGAGCCGACAGT	728
Db	245	AGAGTGTCTGTGTGACCTCTCGAGAGACACAGTGTATAGGCAACAGATATCCAGAGCCGACAGT	304
QY	739	CTAAGCCCGGACCTCTCGAGCCACAGCCGCTGTGCGCCCTTGCGCCAGCGAGCG	798
Db	305	CTAAGCCCGGACCTCTCGAGCCACAGCCGCTGTGCGCCCTTGCGCCAGCGAGCG	364
QY	799	CTTTCACCGGCTTCAGGCCACCTATCCGTACCTTGACACAGAGATGCACTTGCCAC	858
Db	365	CTTTCACCGGCTTCAGGCCACCTATCCGTACCTTGACACAGAGATGCACTTGCCAC	424
QY	859	CATCTGCTGTGACAGCGGGAGAGAGCCCTTACAGAGGCCCTTGACACCTTCCAGCT	918
Db	425	CATCTGCTGTGACAGCGGGAGAGAGCCCTTACAGAGGCCCTTGACACCTTCCAGCT	484
QY	919	TCGGAGACCCCGAGAGAGAGTTGGAATGAAACCGGGAGTGGGTGCGGACCCCAACAG	978
Db	485	TCGGAGACCCCGAGAGAGAGTTGGAATGAAACCGGGAGTGGGTGCGGACCCCAACAG	544
QY	979	AACCATTTTGACAGTACCTGATGTATGTGACAGGCTGGCGGCCCTTGCCGCCAG	1038
Db	545	AACCATTTTGACAGTACCTGATGTATGTGACAGGCTGGCGGCCCTTGCCGCCAG	604
QY	1039	CAGTAACTCGGGACATACAGCCACAGCTGTACAGGCGAGCGGCGCATGAGAGGGGCGCC	1098
Db	605	CAGTAACTCGGGACATACAGCCACAGCTGTACAGGCGAGCGGCGCATGAGAGGGGCGCC	664
QY	1099	GCCCACTTAACGAGAGGTATTCGGCCCACTACCGGGGCTCTCTTCCAGACACAGCAGAG	1158
Db	665	GCCCACTTAACGAGAGGTATTCGGCCCACTACCGGGGCTCTCTTCCAGACACAGCAGAG	724
QY	1159	CAGTGGGCGCCCTCTCTTCTGTGAGGGAGACCGGGCTCCACACACACATGCGCG--CC	1216
Db	725	CAGTGGGCGCCCTCTCTTCTGTGAGGGAGACCGGGCTCCACACACACATGCGCGCC	784
QY	1217	CTAAGAGCGCAG--CCATCTGAGCAAGCAAGAGATGAA-----CAGAAAGCACACCTC	1271
Db	785	CTAAGAGCGCAGCGCCATCTGTAGCAAGCAAGAGATGAAACCGCAAGAGGACACCTTC	844
QY	1272	TC TAGGGTCCCGAGGGGCGCGGGCTGTGGGCTGCG	1306
Db	845	TTCTAGGTCCCGAGGGGCGCGGGCTGTGGG	879
RESULT 12			
BUE02918	850 bp	mrna	linear EST 20-SEP-2002
LOCUS	AGENCOURT 10016502 NIH MGC 142	Homo sapiens	cDNA clone
DEFINITION	IMAGE:6497853 5', mRNA sequence.		
ACCESSION	BUE02918		
VERSION	BUE02918.1	GI:23254677	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
	1 (bases 1 to 850)		
REFERENCE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>		
	Tissue Procurement: NCI		
	cDNA Library Preparation: Michael Brownstein Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	<a href="http://image.lnl.gov">http://image.lnl.gov</a>		
	Plate: L1CM2679	row: 1	column: 22













Db 271 CTCGAGAGACAGTGTCTGAGGCAACGAAATCCAGAGCCGAGGTTCTAGCCGCCGCTCG 330  
Qy 754 GCCACCGACGCTGCGCTGCGCCCTTGGCCCAAGCGGAGCGCTTCCACCGTTTCA 813  
Db 331 GCCACCGACGCTGCGCTGCGCCCTTGGCCCAAGCGGAGCGCTTCCACCGTTTCA 390  
Qy 814 GCCACCGATCGTACCTGACGACGAAATGAACTGCGACCCACCATCTGCTGTGAGA 873  
Db 391 GCCACCTATCTGATCTGACGACGAAATGAACTGCGACCCACCATCTGCTGTGAGA 450  
Qy 874 CGGAGAGAGCGCCCGACCTTACAGAGGCGCTGACCCCTCAAGCTTTCGAGAACCCGAGCA 933  
Db 451 CGGAGAGAGCGCCCGACCTTACAGAGGCGCTGACCCCTCAAGCTTTCGAGAACCCGAGCA 510  
Qy 934 CGAGCTGGAATCTGAACCGGAGAGTGGTGGCGGCAACCCCAAGAGAACTTCTTGACAG 993  
Db 511 GCAGCTGGAATCTGAACCGGAGAGTGGTGGCGGCAACCCCAAGAGAACTTCTTGACAG 570  
Qy 994 TGACCTGATGATTAATGTCAGAGCTGGGGCGCCCTGCGCCCGCCAGACATTAATCTGGGGCAT 1053  
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Qy 1054 CAGCGCACTGTCTACGCGACGCGGCGCATGAGAGGCGCGCCCGACCTTACAGCGA 1113  
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Qy 1174 CTGTGAGAGGAGACCGCGCTCCACACACACATCGGCGCCCTAGAGAGCGACCAT 1233  
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Qy 1234 CTGAGCAAGAAGATTAACAGAAAGACACCTCTTAAAGGTTCCCAAGGGGCGCG 1293  
Db 811 CTGAGCAAGAAGATTAACAGAAAGACACCTCTTAAAGGTTCCCAAGGGGCGCG 870  
Qy 1294 GGCTGGGGCTGCTGAGTGAAGGAGCGAG 1321  
Db 871 GGCTGGGGCTGCTGAGTGAAGGAGCGAG 898

RESULT 2  
US-09-769-482-2  
; Sequence 2, Application US/09769482  
; Patent No. 6566130  
; GENERAL INFORMATION:  
; APPLICANT: SRIVASTAVA, SHIV  
; APPLICANT: MOU, JUD W.  
; APPLICANT: XU, LINDA L.  
; APPLICANT: SEGAWA, TAKEHIKO  
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED  
; FILE REFERENCE: 04995 0057-00000  
; CURRENT APPLICATION NUMBER: US/09/769,482  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,772  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/179,045  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 759  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-769-482-2

Query Match 57.2%; Score 755.8; DB 3; Length 759;  
Best Local Similarity 99.7%; Pred. No. 2.1e-133;  
Matches 757; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 518 ATCAGAGCTGAGATTGTTTCAGATCATCATCTGTGTGTGATGATGATGTG 577  
Db 1 ATGCGGAGAGCTGAGATTGTTTCAGATCATCATCTGTGTGTGATGATGATGTG 60  
Qy 578 GTGTGATCACTGTCTGTGAGCACTTACAGCTGTCTGACGGTCTTTCATCAGCCG 637  
Db 61 GTGTGATCACTGTCTGTGAGCACTTACAGCTGTCTGACGGTCTTTCATCAGCCG 120  
Qy 638 CACAGCCAGGGCGGAGAGAGAAAGATGCTGTCTTCCAGAGGATGCTGTGAGCCCTG 697  
Db 121 CACAGCCAGGGCGGAGAGAGAAAGATGCTGTCTTCCAGAGGATGCTGTGAGCCCTG 180  
Qy 698 GAGAGCAAGTGTACAGCAACGAAATCCAGAGCGCGAGTCTTACGCCCGCTCGGCC 757  
Db 181 GAGAGCAAGTGTACAGCAACGAAATCCAGAGCGCGAGTCTTACGCCCGCTCGGCC 240  
Qy 758 ACCGACCGCTGTGCTGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCCAGCC 817  
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Db 301 ACCTATCCGTACCTGACGACAGATGACCTTCCAGCTTCCAGAGCGCG 360  
Qy 878 GAGAGCGCCCACTTACAGAGCGCGCTTCCAGCTTCCAGAGCGCG 937  
Db 361 GAGAGCGCCCACTTACAGAGCGCGCTTCCAGCTTCCAGAGCGCG 420  
Qy 938 CTGGAATCTGAACCGGAGTGTGTGCGGCACTCCCAAGAGACATCTTTCAGAGTAC 997  
Db 421 CTGGAATCTGAACCGGAGTGTGTGCGGCACTCCCAAGAGACATCTTTCAGAGTAC 480  
Qy 998 CTGATGATGATGTCAGAGCTGGGGCGCGCCCTGCGCCCGCCAGAGTAACTGGGAGTACG 1057  
Db 481 CTGATGATGATGTCAGAGCTGGGGCGCGCCCTGCGCCCGCCAGAGTAACTGGGAGTACG 540  
Qy 1058 GCCAGTGTCTACGCGACGCGGCGCATGAGAGGCGCGCGCCCACTTACAGAGGTC 1117  
Db 541 GCCAGTGTCTACGCGACGCGGCGCATGAGAGGCGCGCGCCCACTTACAGAGGTC 600  
Qy 1118 ATCGGCACTACCGGGGCTCTCTTCCAGACACGAGACAGTGGGGCGCGCTCTT 1177  
Db 601 ATCGGCACTACCGGGGCTCTCTTCCAGACACGAGACAGTGGGGCGCGCTCTT 660  
Qy 1178 CTGAGAGGAGACCGCGCTTCCACACACATGCGGCGCCCTAGAGAGCGAGCATCTG 1237  
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Qy 1238 AGCAAGAGAGATTAACAGAAAGACACCTCTTAA 1276  
Db 721 AGCAAGAGAGATTAACAGAAAGACACCTCTTAA 759

RESULT 3  
US-09-091-952A-7  
; Sequence 7, Application US/09091952A  
; Patent No. 6458532  
; GENERAL INFORMATION:  
; APPLICANT: Detera-Wadleigh, Sevilla D.  
; Gershon, Elliot S.  
; Badner, Judith A.  
; Goldin, Lynn R.  
; Berretini, Wade H.  
; Yoshikawa, Takeo  
; Sanders, Alan R.  
; Esterling, Lisa E.  
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic  
; Tests for Manic-Depressive Illness  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/091,952A  
FILING DATE: 19-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,278  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: PCT/US97/19381  
FILING DATE: 28-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Timothy L.  
REGISTRATION NUMBER: 35,367  
REFERENCE/DOCKET NUMBER: 015280-297100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1...921  
OTHER INFORMATION: Clone 22 coding region  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-091-952A-7

Query Match	Similarity	26.7%	Score 352.2	DB 3	Length 921
Best Local	Similarity 73.1%		Pred. No. 1.9e-57		
Matches	482	Conservative	0	Mismatches 168	Indels 9
					Gaps 2
QY	506	CAGACATGAGATCA	CGGAGCTGAGAGTTGTTTCAGATCATCATATCGTGTGTGATG	565	
DB	166	CCGGGCATCTTCA	CTCGGAGCTGAGATTGGCCCAATCATATCATATCGTGTGTGATG	225	
QY	566	ATGTGATGTGTGTGTGATCA	CGTGCCTGTGAGCCATCAAGCTGTGTGACGGTTC	625	
DB	226	ACGGTGAATGTGTGTGTGATCA	CTGTCTGCCTGTGTAACCACTAACAAAGTCTTCCACGCGGTTC	285	
QY	626	TTTCATCAGCGCGGCAC	AGCCAGGGGGCGGAGAGAAAGATGCCCTGTCTCAGAGAGATGC	685	
DB	286	TTTCATCAACCGCCCGGA	CCAGAGCGGAGAGAGAGAGAGAGGGGTGCGCAGAGAGGGTCC	345	
QY	686	CTGTGAGCCTCGGAGAGCA	CACTGTATAGGCAACCGGATCCAGAGCGCGAGGTCTTACGCC	745	
DB	346	CTGTGGCTTCAGACAGCGCC	CGCACCGCGGGCTGGG-----CGCTGGAGATCATGAT	399	
QY	746	CGGCTTCGGGCCAC	CGGACCGGCTGTGCGCGCCCTTGTGCCACGGGAGCGCTTCCAC	805	
DB	400	GCCCGCGGTCCAGGGGA	CAGGTTTACAGGCGCGTCTTCATCCAGAGGAGTGGCTTCAAC	459	
QY	806	CGCTTCAGGCCCA	CCATTCGATACCGTACCGAGACAGAGATGAGACTGTGCACCCACCATCTGG	865	
DB	460	CGCTTCAACCCCA	CTTACCCCTATGTGCAAGACAGAAATGATTTCTCTCCACATCTTC	519	
QY	866	CTGTGAGAGGGGAGAGCC	CCCACTTACAGAGGCGCTGTGCACTCTTCAGACTTTCGGAGC	925	
DB	520	CTGTCCGAGCGGTGA	AGGCCAAGCTCTTTCACAGGGGCGCTGTGACCTGTGACGCTCGGGAGC	579	
QY	926	CCCGAGCAGACGTGGA	ACTGAAACGGGAGTGTGTGTGCGGCACCCCAACAGACATTC	985	

Db 580 CCTGAAACAGCAGATGGAACCTGAACGAGAGTCCGTGAGAGGCCCAACCCAAACGAAACATA 639

Qy 986 TTTCAGACAGTCACTGATGATATGTCAGAG--CTGGGCGGGCCCTCGGCCCCCAGCAGT 1043

Db 640 TTTCACAGTGTATTAATGACATTGCTATGATATAGCGGGGCTTCATGCCCCAACCGACAGC 699

Qy 1043 AACTCCGGGCATCAACCGCCACGTGCTATGCGGACGCGCGGCGCATGGAAGGGGCGCGGCC 1102

Db 700 AACTCGGGGCATCAGGCAAGCACTCGACAGCACTAAGGAGAGATGAGAGGGGCGACCCCC 759

Qy 1103 AACTACAGCGAGTCATCGGCGCACTATCCCGGGGATCTTCCTTCAGACACAGCAGAGCAG 1161

Db 760 ACATACAGCGAGGTGATGGGCGCACCAACCGAGCGGCTCTTCCTTCATCACAGCGGAG 818

RESULT 4  
 US-09-952A-6  
 Sequence 6, Application US/09091952A  
 Patent No. 6458532  
 GENERAL INFORMATION:  
 APPLICANT: Detera-Wadleigh, Sevilla D.  
 Gershon, Elliot S.  
 Badner, Judith A.  
 Goldin, Lynn R.  
 Beretclini, Wade H.  
 Yoshikawa, Takeo  
 Sanders, Alan R.  
 Beterling, Lisa E.  
 TITLE OF INVENTION: Tests for Manic-Depressive Illness  
 NUMBER OF SEQUENCES: 197  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: PASCSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/091,952A  
 FILING DATE: 19-Apr-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/029,278  
 FILING DATE: 28-OCT-1996  
 APPLICATION NUMBER: PCT/US97/19381  
 FILING DATE: 28-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, Timothy L.  
 REGISTRATION NUMBER: 35,367  
 REFERENCE/DOCKET NUMBER: 015280-297100US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8065 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 1...8065  
 OTHER INFORMATION: Clone 22  
 NAME/KEY: CDS



TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,952A

FILING DATE: 19-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/029,278

FILING DATE: 28-OCT-1996

APPLICATION NUMBER: PCT/US97/19381

FILING DATE: 28-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367

REFERENCE/DOCKET NUMBER: 015280-297100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 867 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..867

OTHER INFORMATION: Clone 22 isoform 2 alternatively spliced coding region

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-091-952A-8

Query Match 21.5%; Score 284.2; DB 3; Length 867; Best Local Similarity 68.7%; Pred. No. 1.2e-44; Matches 453; Conservative 0; Mismatches 143; Indels 63; Gaps 2;

506 CAGAGCATGAGATCAGAGAGCTGAGTTGTTCAAGATCATCATCTGTGTGTGATG 565

166 CCGGCGATTTCACTCGAGAGCTGAGTTGCGCCAATATCATATCTCGTGTGTGTC 225

566 ATGTGATGT 625

226 ACGGTATGT 285

626 TTTCATGAGCGGACAGCGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 685

286 TTTCATGAGCGGACAGCGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 329

686 CTGTGCGCTCGGAGAGACAGTGTGAGGACAGGATCCAGAGCGGAGGCTTACGCC 745

330 -----GCCGAGATCATGAT 345

746 CCGGCTCGGCGCCAGCGAGCGCTGCGCGCTTTCGCCAGCGGAGCGCTTTCAC 805

346 GCCCGCGGTCAGAGGAGAGGATTCACAGCGCGCTTTCATCATCAGAGGATCGCTTTCAC 405

806 CGCTTCCAGCCCACTTATCTGTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAG 865

406 CGCTTCCAGCCCACTTACCCCTATGTGACAGACAGAGATTGATCTTCTCCCATCTCC 465

866 CTGTGACAGCGGAG 925

466 CTGTGACAGCGGAG 525

926 CCGGAG 985

526 CCGGAG 585

986 TTTCATGAGCGGACAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1042

586 TTTCATGAGCGGACAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645

1043 AACTCGGAG 1102

646 AACTCGGAG 705

1103 AACTCGGAG 1161

706 AACTCGGAG 764

RESULT 7

US-09-621-976-2162

Sequence 2162, Application US/09621976

Patent No. 6633963

GENERAL INFORMATION:

APPLICANT: Dumas Mline Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 2162

LENGTH: 391

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 17..223

US-09-621-976-2162

Query Match 6.8%; Score 90.4; DB 3; Length 391; Best Local Similarity 75.7%; Pred. No. 3e-08; Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

1019 GCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1078

26 GCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 85

1079 GCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1138

86 GCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 145

1139 TCTTTCATGAGCGGACAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1166

146 TCTTTCATGAGCGGACAGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 173

RESULT 8

US-09-616-289-48/c

Sequence 48, Application US/09616289

Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING



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/ RESULT 11
/ US-09-976-740-48
/ Sequence 48, Application US/09976740
/ Patent No. 6876817
/ GENERAL INFORMATION:
/ APPLICANT: Lees, Ann M.
/ APPLICANT: Lees, Robert S.
/ APPLICANT: Law, Simon W.
/ APPLICANT: Arjona, Anibal A.
/ TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
/ TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
/ TITLE OF INVENTION: APHROSCLEROSIS
/ FILE REFERENCE: 10797-004001
/ CURRENT APPLICATION NUMBER: US/09/976,740
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 09/616,289
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 08/979,608
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: US 60/031,930
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: US 60/048,547
/ PRIOR FILING DATE: 1997-06-03
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 48
/ LENGTH: 2561
/ TYPE: DNA
/ ORGANISM: Oryctolagus cuniculus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (246)...(1895)
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QY	98	CCTTAGCGGAGAGGCTTAGGCCCCGGGGGAGGGGGGCGCCGGTGGCAGGCCATTTCG	157
Db	24115	GCGAGCCCCCGCGAGGCCCCCGCGAGCCCCCGGAGCCCCCGGAGCCCCCGG	24116
QY	158	GACCCCAACCGGCGGACCTGCGCAGCGCCCCCGGGGCTGCGCAGAGGAGCGGGGGGCG	217
Db	24115	GAGCCCCCGCGAGCCCCCGGCGAGCCCCCGGCGAGCCCCCGGAGCCCCCGCGAG	24056
QY	218	CAGCGAGCGCGGTCCCCGCGCACTAGCCCCCGCGGCGCCCCCGGAACTTGGGGGACCC	277
Db	24055	CCCCCGCGAGCCCCCGCGAGCCCCCGGCGAGCCCCCGGAGCCCCCGCGAGCC	23966
QY	278	GAGCCCGGAGCGGGGGGCGGCTCCCCCGCGCGCGCTCTGTGATCGGGGCCGAG	337





LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 5.2%; Score 68.8; DB 3; Length 4411529;  
Best Local Similarity 49.8%; Pred. No. 0.0014;  
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;

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Db      3942788  GCCGGGCGACGCGCGGCGACCGCGGCAAGAGCGGCGAGTGTGGCCCGCGCGACGCT 3942847
QY      62  GCGCGCGCGCGCGCGCGGAGCGCTCGGAGAACTAGCGGCAAGGCTCAGCCCG 121
Db      3942848  ATCGGTGGGTGGCGCGCGCGGCAAGCGGCAACGCGCGGACGCGGAGTCTGGCGGTGCG 3942907
QY      122  GCGGCAAGCGCGCGCGCGCTGCGAGCCATTTCGGAAGCCACCGCGGGCACTGCCG 180
Db      3942908  GCGGCGCGCGCGCGCGGCGGCAACACGATCCGCGGCAACGCGGCGCAAGAGGT 3942967
QY      181  -ACGCCCCCGGCGCTGCGAGGAGAGCGGCGGCGGCGAGCGGAGCGGTCGCCGCA 239
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QY      240  CTGAGCCCGCGCGCGCGCGGAACTTGGCGGAGCCGAGCCCGGCGAGCGCGGCGCG 299
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QY      300  CCTCCCCCGCGCGCGCTCTCTGCAATGCGGAGCCCAAGCTCCGAGCGCGCGGAGCCC 359
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QY      360  CCGCGCGCGCGCGCGCGGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCTCCATGACC 419
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QY      420  GCTTGATGGGCTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 459
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Search completed: February 28, 2006, 12:29:25  
Job time : 273.59 secs

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Db 181 AGCCCCCGGGGCTCCGAGGGGAGCGGGGGGCGCAGCGGAGCGCGTCCGGCGCAC 240  
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Qy 301 CTTCCCCCGGGGCTCTCTGCAATGCGGGGGCCGAGCTCGGGGGCGGGCGAGCCCC 360  
Db 301 CTTCCCCCGGGGCTCTCTGCAATGCGGGGGCCGAGCTCGGGGGCGGGCGAGCCCC 360  
Qy 361 CCCCCGCGCCCCCGAGCCCCCGCGCGCGCGCGCGCGCGCGCGCTCCAGCACCG 420  
Db 361 CCCCCGCGCCCCCGAGCCCCCGCGCGCGCGCGCGCGCGCGCGCTCCAGCACCG 420  
Qy 421 CTTGATGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
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Qy 481 GTGCAACTGCAAAAGCTTTTGTTCAGAGCATGAGATCAGAGGAGCTGGATTGTCA 540  
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Qy 541 GATCATCATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
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Qy 601 CCACTACAAAGCTGTGCAAGCTCTTCATCAGCCGCGCACAGCCAGGGGCGAGAGAGA 660  
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Qy 661 AAGATGCTGTCTCTGAGAGAGATGCTGTGGGCTCTGAGAGACAGATGTCAGGCAAG 720  
Db 661 AAGATGCTGTCTCTGAGAGAGATGCTGTGGGCTCTGAGAGACAGATGTCAGGCAAG 720  
Qy 721 AATCCAGAGCGGAGCTGACGCGCGCGCTGCGCCACGACCGCTGCGCGCGCGC 780  
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Qy 781 CTTTCCGAGCGGAGCGCTTCCAGCGCTTCCAGCCCTTACCTTCCAGACAGA 840  
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Qy 841 GATTCAGCTGCGACCCCACTCTGCTGCAAGCGGGGAGAGAGAGAGAGAGAGAG 900  
Db 841 GATTCAGCTGCGACCCCACTCTGCTGCAAGCGGGGAGAGAGAGAGAGAGAGAG 900  
Qy 901 CCGCTGCACTGCTGAGCTTGGGAGCCCGAGCGAGCTGGAATGAAACCGGGAGT 960  
Db 901 CCGCTGCACTGCTGAGCTTGGGAGCCCGAGCGAGCTGGAATGAAACCGGGAGT 960  
Qy 961 GCGCGAGCCCGCAAGAACATCTTTCAGACGTGATGATGATGATGATGATGATG 1020  
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Qy 1021 CCGGCCCCGCCCCCGAGAGTAACTGGGCACTGAGCGCGCACTGCTTACGCGCG 1080  
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Qy 1081 GCGCATGAGAGGGGCGCGCGCGCACCTACAGCGAGCTATGCGGCACTAACCGGG 1140  
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Qy 1141 CTTTCCAGCAGCAGAGAGAGTGGGCGCGCTTCTGAGAGGGAGCCCGGCTCCACA 1200  
Db 1141 CTTTCCAGCAGCAGAGAGAGTGGGCGCGCTTCTGAGAGGGAGCCCGGCTCCACA 1200  
Qy 1201 CAGACATGCGCGCGCTTGAAGAGCGAGCATCTGAGAGAGAGAGAGAGAGAGAG 1260  
Db 1201 CAGACATGCGCGCGCTTGAAGAGCGAGCATCTGAGAGAGAGAGAGAGAGAGAG 1260  
Qy 1261 AGGAGACCTCTCTAAGGGTCCCGAGGGGGGCGGGGCTGGGGCTGCTAAGTAAAGGCA 1320  
Db 1261 AGGAGACCTCTCTAAGGGTCCCGAGGGGGGCGGGGCTGGGGCTGCTAAGTAAAGGCA 1320

Qy 1321 G 1321  
Db 1321 G 1321  
RESULT 2  
US-10-241-220-119  
; Sequence 119, Application US/10241220  
; Publication No. US20030148408A1  
; GENERAL INFORMATION:  
; APPLICANT: Frantz, Gretchen  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Phillips, Heidi  
; APPLICANT: Polakis, Paul  
; APPLICANT: Spencer, Susan  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wu, Thomas  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5010R1-US  
; CURRENT APPLICATION NUMBER: US/10/241, 220  
; CURRENT FILING DATE: 2002-12-13  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 119  
; LENGTH: 4839  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-241-220-119

Query Match 93.0%; Score 1229; DB 6; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 8,9e-288;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GGAAGCTAGCGGAGAGAGCTCAAGCCCGGCGGAGCGCGCGCGCTGCGAGCCATT 60  
Qy 153 TTCCGAGCGCACCCCGCGGCACTGCGCAGCCCGCGGGGCTGCGAGAGAGCGCGGG 212  
Db 61 TTCCGAGCGCACCCCGCGGCACTGCGCAGCCCGCGGGGCTGCGAGAGAGCGCGGG 120  
Qy 213 GGGGCGAGCGAGCGGGTCCCGGCACTGAGCCCGGCGGCGCGCGGAACTTGGCGGC 272  
Db 121 GGGGCGAGCGAGCGGGTCCCGGCACTGAGCCCGGCGGCGCGCGGAACTTGGCGGC 180  
Qy 273 GACCCGAGCCCGGAGCGGGGCGCGCTCCCGCGCGCGCTCTGATGCGGGG 332  
Db 181 GACCCGAGCCCGGAGCGGGGCGCGCTCCCGCGCGCGCTCTGATGCGGGG 240  
Qy 333 CCGAGCTCGGGCGCGCGCGCGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCG 392  
Db 241 CCGAGCTCGGGCGCGCGCGCGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCG 300  
Qy 393 GCGGCGCGCGCGCGCGCGCGAGCGCTTGAATGAGGGGTCAACAGCAGCGCGCGCG 452  
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Qy 453 CCGCGGCGAGCCCAATGCTCTGCGAGCTGCAAGCTGCAAAAGCTTTGTTCCAGACA 512  
Db 361 CCGCGGCGAGCCCAATGCTCTGCGAGCTGCAAGCTGCAAAAGCTTTGTTCCAGACA 420  
Qy 513 TGGAGATCAAGAGCTGAGATTGTTTCAGATCATATATGTTGGTGGTATGATGATG 572  
Db 421 TGGAGATCAAGAGCTGAGATTGTTTCAGATCATATATGTTGGTGGTATGATGATG 480  
Qy 573 TGGTGGTGGTATCAAGCGCGCTGAGAGCGCATCAAGCTGTCAGCGCTTCATCA 632  
Db 481 TGGTGGTGGTATCAAGCGCGCTGAGAGCGCATCAAGCTGTCAGCGCTTCATCA 540  
Qy 633 GCGGCGAGCGAGGGGCGAGAGAGAGATGCCCTGTCTCAGAGAGATGCCCTGTGGC 692  
Db 540 GCGGCGAGCGAGGGGCGAGAGAGAGATGCCCTGTCTCAGAGAGATGCCCTGTGGC 692

Db 541 GCCGACACGCCAGGGGCGGAGAGAGATGCCCTGTCTCAGAGAGATGCTGTGAC 600  
Qy 693 CCTCGAGAGCAACAGTGTAGAGCAACGAATCCAGAGCCGAGGTCTACGCCGCCGCTC 752  
Db 601 CCTCGAGAGCAACAGTGTAGAGCAACGAATCCAGAGCCGAGGTCTACGCCGCCGCTC 660  
Qy 753 GGGCCACCGACCGGCTGTGCGCGGCTTGTGCGCCAGCGGAGGCGCTTCAACCGCTTC 812  
Db 661 GGGCCACCGACCGGCTGTGCGCGGCTTGTGCGCCAGCGGAGGCGCTTCAACCGCTTC 720  
Qy 813 AGCCCACTATCGTACCTGACGACGAGATGCACTGTGCAACCACTCTGTGTGAG 872  
Db 721 AGCCCACTATCGTACCTGACGACGAGATGCACTGTGCAACCACTCTGTGTGAG 780  
Qy 873 AGCGGAGAGAGCCCGACCTTACAGGCGCCCTGTGACCCCTTCAAGCTTGGGACCCGAGC 932  
Db 781 AGCGGAGAGAGCCCGACCTTACAGGCGCCCTGTGACCCCTTCAAGCTTGGGACCCGAGC 840  
Qy 933 AGCAGCTGGAATGGAACCGGAGGTGGTGGCGCAACCCCAAGAAACATCTTGACA 992  
Db 841 AGCAGCTGGAATGGAACCGGAGGTGGTGGCGCAACCCCAAGAAACATCTTGACA 900  
Qy 993 GTGACCTGATGATGTGTCAGAGCTGGGCGGCGCCCTGCCCCAGACAGTAACTCGGAGCA 1052  
Db 901 GTGACCTGATGATGTGTCAGAGCTGGGCGGCGCCCTGCCCCAGACAGTAACTCGGAGCA 960  
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Db 1141 TCTGAGACAAAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGCGGCGC 1200  
Qy 1293 GGGCTGGGCTGCTAGTGTGAAAGAGCAG 1321  
Db 1201 GGGCTGGGCTGCTAGTGTGAAAGAGCAG 1229

RESULT 3  
US-10-269-909-84  
Sequence 84, Application US/10269909  
Publication No. US20030180747A1  
GENERAL INFORMATION:  
APPLICANT: HRUBAN, RALPH H.  
APPLICANT: ARGANI, PERHAM  
APPLICANT: JACOBUIO-DONAHUE, CHRISTINE  
APPLICANT: MAITRA, ANIRBAN  
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES  
FILE REFERENCE: 58303 (71699)  
CURRENT APPLICATION NUMBER: US/10/269,909  
CURRENT FILING DATE: 2003-10-11  
PRIOR APPLICATION NUMBER: 60/328,609  
PRIOR FILING DATE: 2001-10-11  
PRIOR APPLICATION NUMBER: 60/332,754  
PRIOR FILING DATE: 2001-11-19  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 84  
LENGTH: 4839  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-269-909-84

Query Match 93.0%; Score 1229; DB 6; Length 4839;

Best Local Similarity 100.0%; Pred. No. 8,9e-288;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAAGGCGAGAGGCTCAGCCCGGCGGAGAGCGGCGCCCGCTGCGAGCCATT 152  
Db 1 GGAAGCTAAGGCGAGAGGCTCAGCCCGGCGGAGAGCGGCGCCCGCTGCGAGCCATT 60  
Qy 153 TTCCGAGCGCACCGCGGCGGCACTGCGAGCCGCCCGGCGGCTGCGAGGAGCGCGG 212  
Db 61 TTCCGAGCGCACCGCGGCGGCACTGCGAGCCGCCCGGCGGCTGCGAGGAGCGCGG 120  
Qy 213 GGGCGAGCGAGCGCGGTCCCGGCACTGAGCCCGCGGCGGCGCCCGGAACTTGGCGC 272  
Db 121 GGGCGAGCGAGCGCGGTCCCGGCACTGAGCCCGCGGCGGCGCCCGGAACTTGGCGC 180  
Qy 273 GACCCGAGCCCGGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 332  
Db 181 GACCCGAGCCCGGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
Qy 333 CCAGCTCGGCGCGCGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392  
Db 241 CCAGCTCGGCGCGCGCGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
Qy 333 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 452  
Db 301 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
Qy 453 CCGCGCGGAGCGCATGTCTCTGCAAGTGTCACTGCAAGCGCTTGTGTTCCAGACA 512  
Db 361 CCGCGCGGAGCGCATGTCTCTGCAAGTGTCACTGCAAGCGCTTGTGTTCCAGACA 420  
Qy 513 TGGAGATACGAGAGTGTGATGTTGTCAGATCATCATGTGTGTGATGATGATGA 572  
Db 421 TGGAGATACGAGAGTGTGATGTTGTCAGATCATCATGTGTGTGATGATGATGA 480  
Qy 573 TGGT 632  
Db 481 TGGT 540  
Qy 633 GCGCGCACCGAGGCGGAGAGAGAGAGATGCTGTCTCTCAAGAGATGCTGTGTG 692  
Db 541 GCGCGCACCGAGGCGGAGAGAGAGATGCTGTGTCTCTCAAGAGATGCTGTGTG 600  
Qy 693 CCTCGAGAGCAACAGTGTCAAGGCAACGAGATCCAGAGCGGCTTCAAGCGCGCTC 752  
Db 601 CCTCGAGAGCAACAGTGTCAAGGCAACGAGATCCAGAGCGGCTTCAAGCGCGCTC 660  
Qy 753 GGGCCACCGACCGGCTGTGCGCGGCTTGTGCGCCAGCGGAGGCGCTTCAACCGCTTC 812  
Db 661 GGGCCACCGACCGGCTGTGCGCGGCTTGTGCGCCAGCGGAGGCGCTTCAACCGCTTC 720  
Qy 813 AGCCCACTATCGTACCTGACGACGAGATGCACTGTGCAACCACTCTGTGTGAG 872  
Db 721 AGCCCACTATCGTACCTGACGACGAGATGCACTGTGCAACCACTCTGTGTGAG 780  
Qy 873 AGCGGAGAGAGCCCGACCTTACAGGCGCCCTGTGACCCCTTCAAGCTTGGGACCCGAGC 932  
Db 781 AGCGGAGAGAGCCCGACCTTACAGGCGCCCTGTGACCCCTTCAAGCTTGGGACCCGAGC 840  
Qy 933 AGCAGCTGGAATGGAACCGGAGGTGGTGGCGCAACCCCAAGAAACATCTTGACA 992  
Db 841 AGCAGCTGGAATGGAACCGGAGGTGGTGGCGCAACCCCAAGAAACATCTTGACA 900  
Qy 993 GTGACCTGATGATGTGTCAGAGCTGGGCGGCGCCCTGCCCCAGACAGTAACTCGGAGCA 1052  
Db 901 GTGACCTGATGATGTGTCAGAGCTGGGCGGCGCCCTGCCCCAGACAGTAACTCGGAGCA 960  
Qy 1053 TCAGCGCCACGTGCTACGGGACGGGCGGCGATGAGAGGCGCGCCGACCTTACAGCG 1112  
Db 961 TCAGCGCCACGTGCTACGGGACGGGCGGCGATGAGAGGCGCGCCGACCTTACAGCG 1020  
Qy 1113 AGGTATCGGCACTACCGGCGGCTCTCTTCCAGACCAAGACAGACATGGGCGCGCT 1172

Db 1021 AGGTATGAGCCACTACCCGGGCTCTCTTCCAGACCAAGAGAGAGTGGCCCT 1080  
Qy 1173 CCTTCTGAGGAGGAGCCCGGCTCCACACACACATGCGCCCTTAAGAGAGGCA 1232  
Db 1081 CCTTCTGAGGAGGAGCCCGGCTCCACACACACATGCGCCCTTAAGAGAGGCA 1140  
Qy 1233 TCTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCC 1292  
Db 1141 TCTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCC 1200  
Qy 1293 GGGCTGGGCTGCTAGTGAAGAGAGAG 1321  
Db 1201 GGGCTGGGCTGCTAGTGAAGAGAGAG 1229

RESULT 4  
US-10-269-909-85  
; Sequence 85, Application US/10269909  
; Publication No. US20030180747A1  
; GENERAL INFORMATION:  
; APPLICANT: HRUBAN, RALPH H.  
; APPLICANT: ARGANI, PEDRAM  
; APPLICANT: IACOBUIZIO-DONAHUE, CHRISTINE  
; APPLICANT: MAITRA, ANIRBAN  
; TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES  
; FILE REFERENCE: 58303(71699)  
; CURRENT APPLICATION NUMBER: US/10/269,909  
; PRIOR FILING DATE: 2003-10-11  
; PRIOR APPLICATION NUMBER: 60/328,609  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/332,754  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 85  
; LENGTH: 4839  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-269-909-85

Query Match 93.0%; Score 1229; DB 6; Length 4839;  
Best Local Similarity 100.0%; Pred. No. 8.9e-288;  
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAGCGGACAGAGCTCAGCCCGGCGAGCGCGCGCCGCTGCGAGCCACT 152  
Db 1 GGAAGCTAGCGGACAGAGCTCAGCCCGGCGAGCGCGCGCGCCGCTGCGAGCCACT 60  
Qy 153 TTCGGAGCGCACCCGCGGACATGCGGAGCGCCCGGGCTGCGAGGGAGGCGGG 212  
Db 61 TTCGGAGCGCACCCGCGGACATGCGGAGCGCCCGGGCTGCGAGGGAGGCGGG 120  
Qy 213 GGGCGAGGAGGAGCGGGGTCGCGGACATGAGCCCGCGGCGCCCGGAACTTGGCGG 272  
Db 121 GGGCGAGGAGGAGCGGGGTCGCGGACATGAGCCCGCGGCGCCCGGAACTTGGCGG 180  
Qy 273 GACCCGAGCCCGGAGCGCGGCGGCTCCCGCGCGCGCGCTCTGCGATGCGGGG 332  
Db 181 GACCCGAGCCCGGAGCGCGGCGGCTCCCGCGCGCGCGCTCTGCGATGCGGGG 240  
Qy 333 CCCAGCTCCGGGCGCGGCGGAGCGCCCGCGCGCGCCCGAGCGCCCGCGCGCG 392  
Db 241 CCCAGCTCCGGGCGCGGCGGAGCGCCCGCGCGCGCCCGAGCGCCCGCGCGCG 300  
Qy 393 GCGCGCGCGCGCGCGGCTCCATGCAACGCTTGAATGGGGGCAAGAGACCGCGCGG 452  
Db 301 GCGCGCGCGCGCGCGGCTCCATGCAACGCTTGAATGGGGGCAAGAGACCGCGCGG 360  
Qy 453 CGCGCGGAGCGCAATGTCTCTCTGCACTGCACTGCAAAAGCTCTTTGTTCCAGAGA 512  
Db 361 CGCGCGGAGCGCAATGTCTCTCTGCACTGCACTGCAAAAGCTCTTTGTTCCAGAGA 420  
Qy 513 TGGAGATCAAGAGAGTGAAGTTTGTTCAGATCATCATGCTGCTGATGATGATGAT 572

Db 421 TGGAGATCAAGAGAGTGAAGTTTGTTCAGATCATCATGCTGCTGATGATGATGAT 480  
Qy 573 TGGTGTGTGTATCATCGTCTGCTGAGCACTACAGCTGTCTGACAGCTCTTATCA 632  
Db 481 TGGTGTGTGTATCATCGTCTGCTGAGCACTACAGCTGTCTGACAGCTCTTATCA 540  
Qy 633 GCGGCAAGCGGAGGCGGAGAGAGATGCTGCTCTGAGAGAGATGCTGTGGC 692  
Db 541 GCGGCAAGCGGAGGCGGAGAGAGATGCTGCTCTGAGAGAGATGCTGTGGC 600  
Qy 693 CCTGAGAGAGAGAGAGTCAAGGCAAGCAATCCAGAGCGGAGAGTCAAGCGCCGCTC 752  
Db 601 CCTGAGAGAGAGAGAGTCAAGGCAAGCAATCCAGAGCGGAGAGTCAAGCGCCGCTC 660  
Qy 753 GGGCCACGAGCGGCTGGGCTGCGCGCCCTTCCCGCGAGCGGAGGCTTCCAGCGCTTC 812  
Db 661 GGGCCACGAGCGGCTGGGCTGCGCGCCCTTCCCGCGAGCGGAGGCTTCCAGCGCTTC 720  
Qy 813 AGCCCACTATTCGTAACCTGAGAGAGAGATGAGATGAGATGAGATGAGATGAGAT 872  
Db 721 AGCCCACTATTCGTAACCTGAGAGAGAGATGAGATGAGATGAGATGAGATGAGAT 780  
Qy 873 AGGGAG 932  
Db 781 AGGGAG 840  
Qy 933 AGCAGCTGGAATGGAACCGGAGAGTGGTGGCGGAGAGAGAGAGAGAGAGAGAGAG 992  
Db 841 AGCAGCTGGAATGGAACCGGAGAGTGGTGGCGGAGAGAGAGAGAGAGAGAGAGAG 900  
Qy 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052  
Db 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Qy 1053 TCAGGCGGAG 1112  
Db 961 TCAGGCGGAG 1020  
Qy 1113 AGGTATGAGCGGACACTACCCGGGCTCTCTTTCAGAGAGAGAGAGAGAGAGAGAG 1172  
Db 1021 AGGTATGAGCGGACACTACCCGGGCTCTCTTTCAGAGAGAGAGAGAGAGAGAGAG 1080  
Qy 1173 CCTTCTGAGGAGGAGCCCGGCTCCACACACACATGCGCCCTTAAGAGAGGCA 1232  
Db 1081 CCTTCTGAGGAGGAGCCCGGCTCCACACACACATGCGCCCTTAAGAGAGGCA 1140  
Qy 1233 TCTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCC 1292  
Db 1141 TCTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGAGTCCCGAGGGGGCC 1200  
Qy 1293 GGGCTGGGCTGCTAGTGAAGAGAGAG 1321  
Db 1201 GGGCTGGGCTGCTAGTGAAGAGAGAG 1229

RESULT 5  
US-10-872-972-119  
; Sequence 119, Application US/10872972  
; Publication No. US20040229277A1  
; GENERAL INFORMATION:  
; APPLICANT: Franz, Gretchen  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Phillips, Heidi  
; APPLICANT: Polakis, Paul  
; APPLICANT: Spencer, Susan  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wu, Thomas  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5010R1-US  
; CURRENT APPLICATION NUMBER: US/10/872,972



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?
?
? CURRENT FILING DATE: 2004-06-21
? PRIOR APPLICATION NUMBER: US/10/241,220
? PRIOR FILING DATE: 2002-09-11
? NUMBER OF SEQ ID NOS: 120
?
? SEQ ID NO 119
?
? LENGTH: 4835
?
? TYPE: DNA
?
? ORGANISM: Homo Sapien
?
? US-10-872-972-119

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Query Match	93.0%;	Score 1229;	DB 8;	Length 4839;
Best Local Similarity	-100.0%;	Pred. No. 8.9e-288;		
Matches 1229; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

OY	93	GGAAAGCTAAGCGGCAAGAGGCTCAGGCGCCGGGCGAGCGCGCCCGCTGCGACGCCATT	152
Db	1	GGAAAGCTAAGCGGCAAGAGGCTCAGGCGCCGGGCGAGCGCGCCCGCTGCGACGCCATT	60
OY	153	TTCCGGAAGCCACCCCGGGGACCTGCGACGCGCCCGGGGCTGCGAGGGAGAGCCGGG	212
Db	61	TTCCGGAAGCCACCCCGGGGACCTGCGACGCGCCCGGGGCTGCGAGGGAGAGCCGGG	120
OY	213	GGGGCGCAGCGGAGCGCGGTCCCGCGCAGCGACCGCGGGCGCCCGGGGAACTTGGCGGG	272
Db	121	GGGGCGCAGCGGAGCGCGGTCCCGCGCAGCGACCGCGGGCGCCCGGGGAACTTGGCGGG	180
OY	273	GACCCGAGGCCGCGAGCGGGGGCGGCTCCCGCGCGCGGCTCTTGATGCGGGGCG	332
Db	181	GACCCGAGGCCGCGAGCGGGGGCGGCTCCCGCGCGCGGCTCTTGATGCGGGGCG	240
OY	333	CCCAAGCTCCGGGCGCGGCGCGAGGACCCCGCGGCGCGCGCGCGCGCGCGCG	392
Db	241	CCCAAGCTCCGGGCGCGGCGCGAGGACCCCGCGGCGCGCGCGCGCGCGCGCGCG	300
OY	393	GCGGCGCGCGCGCGCGCTCATGACCGCTTGATGGGGGTCAACACACCGCGCGCGCG	452
Db	301	GCGGCGCGCGCGCGCGCTCATGACCGCTTGATGGGGGTCAACACACCGCGCGCGCG	360
OY	453	CCGCGGGGAGGCCCAATGTTCTCTCTGACGTCACCTGCAACGCTCTTTGTTCAAGACA	512
Db	361	CCGCGGGGAGGCCCAATGTTCTCTCTGACGTCACCTGCAACGCTCTTTGTTCAAGACA	420
OY	513	TGGAGATCAACGAGCGTGGAGTTTGTTCAATATCATATCATCGGGGGATGATAGTGA	572
Db	421	TGGAGATCAACGAGCGTGGAGTTTGTTCAATATCATATCGGGGGATGATAGTGA	480
OY	573	TGATGTGTGTGATCAAGTGCCTGCTGAGGCCATTACAAGCTGTCTGACCGTCCCTTCATCA	632
Db	481	TGATGTGTGTGATCAAGTGCCTGCTGAGGCCATTACAAGCTGTCTGACCGTCCCTTCATCA	540
OY	633	GCGCGGACACGCCAGGGGGCGAGAGAGAAATGCTGTCTTCAAGAAAGATGCTGTGGC	692
Db	541	GCGCGGACACGCCAGGGGGCGAGAGAGAAATGCTGTCTTCAAGAAAGATGCTGTGGC	600
OY	693	CCTCGGAGAGCACAAGTGTCAAGGACGGAATCCCAAGCCGACAGGTCTAGGCCGCCGCTC	752
Db	601	CCTCGGAGAGCACAAGTGTCAAGGACGGAATCCCAAGCCGACAGGTCTAGGCCGCCGCTC	660
OY	753	GGCCCAACCGACCGGCTGGCGGTGCGGCTTGTGCGCAGCGGGAGCGCTTTCACCGCTTC	812
Db	661	GGCCCAACCGACCGGCTGGCGGTGCGGCTTGTGCGCAGCGGGAGCGCTTTCACCGCTTC	720
OY	813	AAGCCCACTTATCCGTATCTTGACAGCAGAGATGGAACCTGACACCCACATCTGCTGACG	872
Db	721	AAGCCCACTTATCCGTATCTTGACAGCAGAGATGGAACCTGACACCCACATCTGCTGACG	780
OY	873	ACGGGGAGAGGCCCCACCTTACAGAGGCCCTTGCACCTTCAGCTTGGGAACCCGAGC	932
Db	781	ACGGGGAGAGGCCCCACCTTACAGAGGCCCTTGCACCTTCAGCTTGGGAACCCGAGC	840
OY	933	AGCAGCTGGAACCTGAAACCGGGAGATCGTGGCGCACCCCAACAGAACATCTTGGACA	992
Db	841	AGCAGCTGGAACCTGAAACCGGGAGATCGTGGCGCACCCCAACAGAACATCTTGGACA	900

Qy	993	GTGACCTGGATGGAATGAGTCCAGAGGTCTGGGCGGGCCCTGTCGCCCCCGACGAGTAACTCGGAGCA	1052
Db	901	GTGACCTGGATGGAATGAGTCCAGAGGTCTGGGCGGGCCCTGTCGCCCCCGACGAGTAACTCGGAGCA	960
Qy	1053	TCACGCGCACGTCGCTTACGCGAGCGGCGGGGCGCAGTGAAGGAGGCGCGCGCCACTTACACG	1112
Db	961	TCAGCGCCACGTGCTTACGCGAGCGGCGGGGCGCAGTGAAGGAGGCGCGCGCCACTTACACG	1020
Qy	1113	AGGTCAATCGGCACTACCCCGGGGTCTCTCTTCCAGCACACAGCAGAGCATGTGGGCGGCTCT	1172
Db	1021	AGGTCAATCGGCACTACCCCGGGGTCTCTCTTCCAGCACACAGCAGAGCATGTGGGCGGCTCT	1080
Qy	1173	CCTTGTCTGAGAGGGGACCCCGGCTCCACACACACATCGGCGCCCTGAGAGGCGGACGCA	1232
Db	1081	CCTTGTCTGAGAGGGGACCCCGGCTCCACACACACATCGGCGCCCTGAGAGGCGGACGCA	1140
Qy	1233	TCTGAGCAAAAGAGAGGATTTAAACAGAAAGGACACCTCTCTAGGATCCCGAGGGGGGCC	1292
Db	1141	TCTGAGCAAAAGAGAGGATTTAAACAGAAAGGACACCTCTCTAGGATCCCGAGGGGGGCC	1200
Qy	1293	GGGCTGGGGCTGCCTAGGTTAAAAAGGCGAG	1321
Db	1201	GGGCTGGGGCTGCCTAGGTTAAAAAGGCGAG	1229

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RESULT 6
US-10-872-991-119
/ Sequence 119: Application US/10872991
/ Publication No. US20040242860A1
/ GENERAL INFORMATION:
/ APPLICANT: Frantz, Gretchen
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Phillips, Heidi
/ APPLICANT: Polakis, Paul
/ APPLICANT: Spencer, Susan
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wu, Thomas
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ TITLE OF INVENTION: TREATMENT OF TUMOR
/ FILE REFERENCE: P5010R1-US
/ CURRENT APPLICATION NUMBER: US/10/872,991
/ CURRENT FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: US/10/241,220
/ PRIOR FILING DATE: 2002-09-11
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 119
/ LENGTH: 4839
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-872-991-119

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Query Match	93.0%: Score 1229; DB 8; Length 4839;
Best Local Similarity	100.0%: Pred. No. 8.9e-268; Mismatches 0; Indels 0; Gaps 0;
Matches 1229; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	93 GGAAGCTAGGCGGAGAGCTCAGCCCGCGCGAGCGCGCCCGCTGCAGCCATT 152
Db	1 GGAAGCTAGGCGGAGAGCTCAGCCCGCGCGAGCGCGCCCGCTGCAGCCATT 60
QY	153 TTCCGAGAGCCACCCGCGGCGACTCCCGAGCCCGCGCGGCTGCGGAGGAGCGCGGAG 212
Db	61 TTCGAGAGCCACCCGCGGCGACTCCCGAGCCCGCGCGGCTGCGGAGGAGCGCGGAG 120
QY	213 GGGCGAGCGGAGCGCGCTCCCGGCACTGAGCCCGCGGCGGCGCCCGGAAACTTGGCGG 272
Db	121 GGGCGAGCGGAGCGCGGCTCCCGGCACTGAGCCCGCGGCGGCGCCCGGAACTTGGCGG 180
QY	273 GACCCGAGCCCGGAGAGCGCGGCGCGCGCTCCCGCGCGCGCGCTCTGTGATGGGGGG 332
Db	181 GACCCGAGCCCGGAGAGCGCGGCGCGCGCTCCCGCGCGCGCGCTCTGTGATGGGGGG 240





[illegible]

PRIOR APPLICATION NUMBER: 09/599,596  
PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 09/630,334  
 PRIOR FILING DATE: 2000-07-31  
 PRIOR APPLICATION NUMBER: 09/606,565  
 PRIOR FILING DATE: 2000-06-29  
 PRIOR APPLICATION NUMBER: 09/606,317  
 PRIOR FILING DATE: 2000-06-29  
 PRIOR APPLICATION NUMBER: 09/665,666  
 PRIOR FILING DATE: 2000-09-20  
 PRIOR APPLICATION NUMBER: 09/677,751  
 PRIOR FILING DATE: 2000-09-30  
 NUMBER OF SEQ ID NOS: 162  
 SEQ ID NO 55  
 LENGTH: 969  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (6)...(761)  
 US-09-796-753-55

Query Match 60.8%; Score 803.2; DB 3; Length 969;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-184;  
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

514 GGAAGATCAGGAGCTGAGTTGTTGATCATCATCATCTGAGTGTGATGATGAT 573  
 2 GGAAGATGCGGAGCTGAGTTGTTGATCATCATCATCTGAGTGTGATGATGAT 61  
 574 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633  
 62 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121  
 634 CCGGACAGCCAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693  
 122 CCGGACAGCCAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181  
 694 CTGAG 753  
 182 CTGAG 241  
 754 GCCCAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813  
 242 GCCCAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301  
 814 GCCCAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873  
 302 GCCCAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
 874 CCGGAG 933  
 362 CCGGAG 421  
 934 GCAGCTGAG 993  
 422 GCAGCTGAG 481  
 994 TGAAGCTGAG 1053  
 482 TGAAGCTGAG 541  
 1054 CAGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113  
 542 CAGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601  
 1114 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173  
 602 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661  
 1174 CTGTGTGAG 1233  
 662 CTGTGTGAG 721  
 1234 CTGTGTGAG 1293

Db 722 CTGAGCAAGAGAGAGATTAACAGAAAGACACCTCTAGAGGTCCCGAGGCGCG 781  
 1294 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321  
 Db 782 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809

RESULT 11  
 US-10-205-823-412  
 Sequence 412, Application US/10205823  
 Publication No. US20030108963A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert  
 APPLICANT: Monahan, John E.  
 APPLICANT: Endege, Wilson O.  
 APPLICANT: Gannavarapu, Manjula  
 APPLICANT: Gorbacheva, Bella  
 APPLICANT: Hoersch, Sebastian  
 APPLICANT: Kamatkar, Shubhangi  
 APPLICANT: Monney, Angela M.  
 APPLICANT: Glatt, Karen  
 APPLICANT: Zhao, Xumei  
 APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325,020

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/341,746

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362,158

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 412

LENGTH: 1141

TYPE: DNA

ORGANISM: Homo sapiens

US-10-205-823-412

Query Match 60.7%; Score 802.2; DB 5; Length 1141;  
 Best Local Similarity 98.4%; Pred. No. 1.9e-184;  
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499 TTTGTTCCAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 558  
 77 TTTGTTCCAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 136  
 559 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618  
 137 GGTGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 196  
 619 AGGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 678  
 197 AGGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 256  
 257 AGGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316  
 739 CTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798  
 317 CTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376  
 799 CTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 858





APPLICANT: Glatt, Karen  
 APPLICANT: Zhao, Xumei  
 APPLICANT: Anderson, Duethin  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
 TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
 FILE REFERENCE: MRI-044  
 CURRENT APPLICATION NUMBER: US/11/051,454  
 CURRENT FILING DATE: 2005-02-04  
 PRIOR APPLICATION NUMBER: US/10/205,823  
 PRIOR FILING DATE: 2002-07-25  
 PRIOR APPLICATION NUMBER: 60/307,982  
 PRIOR FILING DATE: 2001-07-25  
 PRIOR APPLICATION NUMBER: 60/314,356  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 60/325,020  
 PRIOR FILING DATE: 2001-09-25  
 PRIOR APPLICATION NUMBER: 60/341,746  
 PRIOR FILING DATE: 2001-12-12  
 PRIOR APPLICATION NUMBER: 60/362,158  
 PRIOR FILING DATE: 2002-03-05  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 412  
 LENGTH: 1141  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-11-051-454-412

Query Match 60.7%; Score 802.2; DB 10; Length 1141;  
 Best Local Similarity 98.4%; Pred. No. 1.9e-184;  
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

499 TTTGTTCCAGAGCATGAGATCAAGAGCTGAGTTGTTGATCATCATCATCGTGT 558  
 77 TCTCTCGGAAACAGAGCATGAGAGCTGAGTTGTTGATCATCATCATCGTGT 136  
 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618  
 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196  
 619 AGGTCCTTCATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678  
 197 AGGTCCTTCATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256  
 679 AGGATGCTGTGAGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738  
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RESULT 14  
 US-10-241-220-44  
 Sequence 44, Application US/10241220  
 Publication No. US20030148408A1  
 GENERAL INFORMATION:  
 APPLICANT: Prant, Gretchen  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Phillips, Heidi  
 APPLICANT: Polakis, Paul  
 APPLICANT: Spencer, Susan  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wu, Thomas  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
 TITLE OF INVENTION: TREATMENT OF TUMOR  
 FILE REFERENCE: P501081-US  
 CURRENT APPLICATION NUMBER: US/10/241,220  
 CURRENT FILING DATE: 2002-12-13  
 NUMBER OF SEQ ID NOS: 120  
 SEQ ID NO 44  
 LENGTH: 1850  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-241-220-44

Query Match 60.7%; Score 802.2; DB 6; Length 1850;  
 Best Local Similarity 98.4%; Pred. No. 1.9e-184;  
 Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:34:50 ; Search time 1731.47 Seconds  
(without alignments)  
1626.862 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321  
Sequence: 1 cgaccgcgctctcgagcgcga.....ctgcgtagtgtaaacgcag 1321

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.New:\*  
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10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq4:\*  
13: /cgn2\_6/ptodata/2/pubpna/US66\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	802.2	60.7	1141	12 US-11-186-284-208	Sequence 208, App
2	128	9.7	129	8 US-10-310-914A-7163	Sequence 7163, App
3	97	7.3	97	8 US-10-310-914A-6542	Sequence 6542, App
4	95.4	7.2	97	8 US-10-310-914A-1107	Sequence 1107, App
5	87.6	6.6	94	8 US-10-310-914A-1106	Sequence 1106, App
6	69.2	5.2	16917	12 US-11-124-367A-5000	Sequence 5000, App
7	68.8	5.2	16917	12 US-11-052-554A-529	Sequence 529, App
8	68.2	5.2	2600	6 US-09-925-065A-92367	Sequence 92367, App
9	67	5.1	1608	6 US-09-925-065A-37513	Sequence 37513, App
10	67	5.1	1608	6 US-09-925-065A-37514	Sequence 37514, App
11	67	5.1	1608	6 US-09-925-065A-37515	Sequence 37515, App
12	67	5.1	2600	6 US-09-925-065A-92368	Sequence 92368, App
13	67	5.1	3240	12 US-11-052-554A-529	Sequence 529, App
14	65.8	5.0	2136	12 US-11-052-554A-539	Sequence 539, App
15	65.6	5.0	191684	12 US-11-121-086-2	Sequence 2, App1
16	65.4	5.0	2562	12 US-11-052-554A-533	Sequence 533, App
17	63.6	4.8	191684	12 US-11-121-086-2	Sequence 2, App1
18	63.4	4.8	23187	9 US-11-236-198-1	Sequence 1, App1
19	63	4.8	1966	7 US-10-506-766-1	Sequence 1, App1
20	63	4.8	2584	8 US-10-821-234-836	Sequence 836, App

21	62.8	4.8	2072	12 US-11-136-527-2747	Sequence 2747, App
22	61.6	4.7	2954	8 US-11-241-347-2	Sequence 2, App1
23	61.6	4.7	18138	8 US-10-995-561-13385	Sequence 13385, App
24	61.4	4.6	18163	8 US-10-310-914A-7162	Sequence 7162, App
25	61.4	4.6	2250	12 US-11-052-554A-532	Sequence 532, App
26	61.2	4.6	26868	8 US-10-933-025-42	Sequence 22, App1
27	61	4.6	153376	12 US-11-121-086-5	Sequence 5, App1
28	61	4.6	172543	12 US-11-121-086-6	Sequence 6, App1
29	60.8	4.6	2825	12 US-11-136-527-192	Sequence 192, App
30	60.4	4.6	2514	12 US-11-052-554A-543	Sequence 543, App
31	60.2	4.6	1609	6 US-09-925-065A-9327	Sequence 9327, App
32	60.2	4.6	1609	6 US-09-925-065A-9328	Sequence 9328, App
33	60	4.5	170995	12 US-11-121-086-35	Sequence 35, App1
34	59.8	4.5	3167	8 US-09-925-065A-21764	Sequence 21764, App
35	59.6	4.5	4739	8 US-10-770-726-2	Sequence 2, App1
36	59.4	4.5	3234	12 US-11-121-438-9	Sequence 9, App1
37	59.4	4.5	10968	12 US-11-075-185-35	Sequence 35, App1
38	59.4	4.5	78869	12 US-11-075-185-1	Sequence 1, App1
39	59.4	4.5	165857	12 US-11-121-086-34	Sequence 34, App1
40	59.2	4.5	9406	12 US-11-136-527-748	Sequence 748, App
41	59.2	4.5	16917	12 US-11-124-367A-5000	Sequence 5000, App
42	59	4.5	1609	6 US-09-925-065A-9329	Sequence 9329, App
43	59	4.5	12277	8 US-10-477-507A-3	Sequence 3, App1
44	58.8	4.5	2406	12 US-11-052-554A-550	Sequence 550, App
45	58.2	4.4	3081	8 US-10-514-863-1	Sequence 1, App1

## ALIGNMENTS

RESULT 1  
US-11-186-284-208  
Sequence 208, Application US/11186284  
Publication No. US20050266493A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Berger, Allison  
APPLICANT: Guillemette, Tracy L.  
APPLICANT: Kametkar, Shubhangi  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Thibodeau, Stephen N.  
APPLICANT: Burgart, Lawrence J.  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MPW01-029P2RNM  
CURRENT APPLICATION NUMBER: US/11/186,284  
CURRENT FILING DATE: 2005-07-21  
PRIOR APPLICATION NUMBER: US/10/301,822  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 60/339,971  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: US 60/361,978  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/381,988  
PRIOR FILING DATE: 2002-05-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 208  
LENGTH: 1141  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (96) ... (854)  
US-11-186-284-208  
Query Match 60.7%; Score 802.2; DB 12; length 1141;  
Best Local Similarity 98.4%; Pred. No. 4.5e-160;  
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
499 TTGTTCCAGACGATGAGATCATCGAGGTGAGTTGTTGATCATCATCATCGTGT 558

Db	77	TTCTCTGGGAAACGAGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCATCTGTGGT	136
QY	559	GGTGTATGATGGTATGGTGGTGGTATCACTGGTGGCTGCTGAGCCCTACAAAGTGTCTGG	618
Db	137	GGTGTATGATGGTATGGTGGTGGTATCACTGGTGGCTGCTGAGCCCTACAAAGTGTCTGG	196
QY	619	AAGGTCCTTCATCAACCGGCAACGCGAGGGGGGAGAGAGAAAGATGGCCCTTCTCTAGA	678
Db	197	AAGGTCCTTCATCAACCGGCAACGCGAGGGGGGAGAGAGAAAGATGGCCCTTCTCTAGA	256
QY	679	AGGATGCTGTGGCCCTCGAGAGCAAGTGTCAAGCAACGAAATCCAGAGCCGAGGT	738
Db	257	AGGATGCTGTGGCCCTCGAGAGCAAGTGTCAAGCAACGAAATCCAGAGCCGAGGT	316
QY	739	CTAGCGCCCGGCTCGAGCCCAACGACCGGCTGGCCGTGCCCTTTCGCCCAAGCGGAGCG	798
Db	317	CTAGCGCCCGGCTCGAGCCCAACGACCGGCTGGCCGTGCCCTTTCGCCCAAGCGGAGCG	376
QY	799	CTTCCACCGGCTTCAGAGCCCACTATCCGTAAGTGTGAGCAACGAGATTCAGTCCCAAC	858
Db	377	CTTCCACCGGCTTCAGAGCCCACTATCCGTAAGTGTGAGCAACGAGATTCAGTCCCAAC	436
QY	859	CATCTCGGCTGTGAGCGGGGAGAGGCCCACTTACAGAGGCCCTGTGCAACCTCGAGCT	918
Db	437	CATCTCGGCTGTGAGCGGGGAGAGGCCCACTTACAGAGGCCCTGTGCAACCTCGAGCT	496
QY	919	TCGGGACCCCGAGCAGCAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA	978
Db	497	TCGGGACCCCGAGCAGCAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA	556
QY	979	AAACCATCTTTCGACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG	1038
Db	557	AAACCATCTTTCGACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG	616
QY	1039	CAGTAACTTCGGGCATTCAGCGCCACGTCGTAACGGCAGCGCGCGGCGATGAGAGGGCGGC	1098
Db	617	CAGTAACTTCGGGCATTCAGCGCCACGTCGTAACGGCAGCGCGCGGCGATGAGAGGGCGGC	676
QY	1099	GCCCACTTACAGCAGAGTTCATCGGCACCTAACCCGGGGTCTCTCTTTCAGACACAGCAGAG	1158
Db	677	GCCCACTTACAGCAGAGTTCATCGGCACCTAACCCGGGGTCTCTCTTTCAGACACAGCAGAG	736
QY	1159	CAGTGGGCGGCCCTCTTTCGTAAGGGGAGCCCGGCTCCACACACACACATCGCGCCCT	1218
Db	737	CAGTGGGCGGCCCTCTTTCGTAAGGGGAGCCCGGCTCCACACACACACATCGCGCCCT	796
QY	1219	AGAGAGCGCAGCCTTTCGAGCAAGAGAAAGATTAACAGAAAGACACCTCTTCTAGGG	1278
Db	797	AGAGAGCGCAGCCTTTCGAGCAAGAGAAAGATTAACAGAAAGACACCTCTTCTAGGG	856
QY	1279	TTCCCAAGGGGGGCGGGGCTGGGGCTGCGTAGGTAAGAAAGGACG	1321
Db	857	TTCCCAAGGGGGGCGGGGCTGGGGCTGCGTAGGTAAGAAAGGACG	899

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RESULT 2
US-10-310-914A-7163/C
; Sequence 7163, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 7163
; LENGTH: 129
; TYPE: RNA

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RESULT 3
US-10-310-914A-6542/C
; Sequence 6542, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200, CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6542
; LENGTH: 97
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-6542

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[illegible]

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RESULT 4
US-10-310-914A-1107/c
; Sequence 1107, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200, CPUS01
; CURRENT APPLICATION NUMBER: US/10/310, 914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1107
; LENGTH: 97
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1107

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RESULT 7
US-11-052-554A-529
; Sequence 529, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIORITY FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 529
; LENGTH: 3240
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-529

Query Match      5.2%; Score 68.8; DB 12; Length 3240;
Best Local Similarity 49.8%; Pred. No. 1.2e-05;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;

QY      2  GACCGGCTCTGCGAGCGAACCCTGATCTCTTGACCTTGAAATGAGAGAGAGAGCGGC 61
DB      1069 GCTCGGCGGAGACGCGCGACCGCGCGAGAGCGGAGCGAGTGTGGCGCGCGGACGCT 1128
QY      62  GCGCGCGCGCGCGCGCGCGCGCTGCGCTGCGGAAAGCTTGGCGGACAGAGCTTCAAGCCCG 121
DB      1129 ATCGGTGGGTGCGCGCGCGCGCAAGGCGCGCAACGCGCGAGAGTCCGCGGTGCG 1188
QY      122  GCGGCGAGCGCGCGCGCGCGCTGCGACGCTTTTCCGAGAGCGGACCGCGCGGACGTGCGG- 180
DB      1189 GCGCGGCGCGCGCGCGCGCGCGCAACACAGTCCGCGCGGCAACGCGCGGCAAGAGGT 1248
QY      181  -ACGCGCGCGCGCGCTTCCAGAGGAGAGCGCGGCGCGAGCGAGCGGCTCCGCGCA 239
DB      1249 CAAAGCGGAGCGGTGTGTGCGGTGGGCGCGCGCGCGCGCGCGCGGTGGCGCGCT 1308
QY      240  CTGAGCGCGCGCGCGCGCGCGGAACTTGGCGCGGACCGGACCGCGCGAGCGCGGCGCG 299
DB      1309 AACGGACCGCTGGCAACGCGGCGCAAGGCGGTGGCGCGGACCGCGCGCGCGCGCA 1368
QY      300  CTTCCCGCGCGCGCGCTTCTGCAATGCGGCGCGCGGACGCTCCGCGCGCGCGGAGCGCC 359
DB      1369 GCTCTCTCACTAACCAAGCGCGGACGCGCGGCGCGG--CGGCAACGAGGCGAGCGG 1426
QY      360  CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATGCAACC 419
DB      1427 GCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1486
QY      420  GCTTGATGGGCTCAACAGACCGCGCGCGCGCGCGCG 459
DB      1487 GCGGACAGGTGGCCAGGCGGCGCGCGCGGTCCCG 1526

RESULT 8
US-09-925-065A-92367/C
; Sequence 92367, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIORITY FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 92367
; LENGTH: 2600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(2600)
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-92367

Query Match      5.2%; Score 68.2; DB 6; Length 2600;
Best Local Similarity 49.6%; Pred. No. 1.6e-05;
Matches 200; Conservative 1; Mismatches 199; Indels 3; Gaps 1;

QY      59  GCGCGCGCGCGCGCGCGCGCGCTGCGGAGGAAAGCTAGCGGACAGAGCTCAAGCC 118
DB      1422 GCTTCGCGCGGTGGGAGGAGAGAGGTTTCGAGGAGCTGCGCGGACGCTCGCGCGG 1363
QY      119  CCGCGCGAGCGCGCGCGCGCGCTGCGACCCATTTTCCGAGCGCACCGCGGCACTGC 178
DB      1362 GCGGTGTGGGAGAGCCSGGGAGTGCAGAGGCGCGGTGCGCGCGCGGATGCGCG 1303
QY      179  CGAGCGCGCGCGCTGCGGAGGAGCGCGGCGCGCGCGAGCGAGCGGTCTCCCGCGC 238
DB      1302 CGGTCCGCGCGCGCGGTGAGGCGCGCGCGGTGTGTCCGCGCGCGGTCCGCGCGCTC 1243
QY      239  ACTAGCGCGCGCGCGCGCGCGCGGAACTTGGGAGGAGCGGACCGGCGCGAGCGGCGGCGC 298
DB      1242 GAGGGGTCCCGGTGCGTCCCTTCCCGCGCGCGCTTTCTGTGCGCTTCCCGTGC 1183
QY      299  GCTTCCCGCGCGCGCGCTCTCTT---CATGCGGCGCGCACTTCCGCGCGCGCGCGCA 355
DB      1182 CCGCGCTTCCCGGTGTCTGTGTCTTCCCGCGCGCTTCCGAAACCGGATCGCG 1123
QY      356  GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCATG 415
DB      1122 GTTCCCGGCGCTCTGCTTCCCGCGCGCGCGCGCGCGCTTCCCGAGGCGTCCGTC 1063
QY      416  CACGCTTGATGGGCTCAACAGACCGCGCGCGCGCGCGCG 458
DB      1062 CCGGCGTGGCGTGGGAGAGCCGTCTTCCCGGTGCG 1020

RESULT 9
US-09-925-065A-37513/C
; Sequence 37513, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIORITY FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
```

	Query Match	5.1%;	Score 67;	DB 6;	Length 1608;
	Best Local Similarity	49.6%;	Pred. No. 2.9e-05;		
	Matches 200;	Conservative	0;	Mismatches 200;	Indels 3; Gaps 1
Qy	59 GGCGGCGGCGCGCGCGCGAGCGCTCGGGTGGGGAAGCTAGCGGCAGAGAGCTCAGCC				118
Dd	430 GCCTGCCGCCGTGCCGGGAGAGACGTTTCGGGGGACCGGCCGCACTGCCGCGCGG				371
Qy	119 CCGGCGGCAAGCGGCGCCCGCTGCCAGGCCATTTCGCGAACGCCACC CGCGGCACTGC				178
Dd	370 GCCGTGTGGGGAGACCGCGGGGATCGCCAGGCGCGGTGGCGCCCGCGGGTGCCCG				311

QY 179 CGACGCCCCCGGCGCTGCGGAGGAGCGCGGGGGGGCGCAGCGGAGCGGCTCCCGGC 238  
DB 310 CGGTCCCGCGGCGGCGGTGAGGCCCCCGCGCGTGTCTCCGCGCGCGGTCCGCGGC 251  
QY 239 ACTGAGCCCCCGGCGGCGCCCGGGAACTTGGCGGCACTCCGAGCCCGGCGAGCGCGGCGC 298  
DB 250 GAGGGGTCCCGCGGTGCGGTCTCCCTTCCCGCGCGCGCGCTTTCTCGGCGCTTCCCGTGC 191  
QY 299 GCTTCCCGCGGCGCGGCTCTGCTG---CATGCGGGGCGCCAGCTCCGGGCGCGCGCGA 355  
DB 190 CCGGCGCTTCCCGCGGTGTCTGTCTTCTTCTCCGCGCGCGCTTCTCGAAGCGGGTCCGCG 131  
QY 356 GCTCATG 415  
DB 130 GGTCCCGCGGCGGCGCTTCTTCCGCGCGCTGCGCGCGCGCTTCCCGGAGCGTCCGTC 71  
QY 416 CACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGC 458  
DB 70 CCGGCGGTCCGCGGTGCGGAGAGCCCGTCTCCCGCGGTGCGG 28

## RESULT 12

US-09-925-065A-92368/c  
; Sequence 92368, Application US/09925065A  
; Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 92368

LENGTH: 2600

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(2600)

OTHER INFORMATION: n = A,T,C or G

US-09-925-065A-92368

Query Match 5.1%; Score 67; DB 6; Length 2600;

Best Local Similarity 49.6%; Pred. No. 2.9e-05;

Matches 200; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 59 GCGCGGCGGCGCGCGCGCGCGCGCGCTGCGCTGGGAGAACTTGGCGGCGGAGAGCTCATGCC 118  
DB 1422 GCTTGGGCGGCGGTGCGGGGAGAGAGCGTTCGGGGGAGACCGGCGCGACTGCGGGGCGG 1363  
QY 119 CCGGCGGAGCGCGCGCGCGCGCTGCGAGCCATTTCGAGACGCCACCGCGGGGCACTGC 178  
DB 1362 GCGGTGTGGGAGAGCGCGCGGGGATGCGCGAGGGCGGTGCGCGCGCGCGGGTGCAGG 1303  
QY 179 CGAGCGCGCGCGCGCGCGCGCGCGAGGAGCGCGGGGGCGAGCGGAGCGCGTCCCGCGC 238  
DB 1302 CCGTGGCGCGCGCGCGGTGAGAGCGCGCGCGGTCTCCCGCGCGGTGCGCGCGCTC 1243  
QY 239 ACTGAGCCCGCGCGCGCGCGCGGAGACTTGGCGGCGAGCCGAGCGCGGCGAGCGGGCGC 298  
DB 1242 GAGGGGTCCCGGTGGGTCTTCCCGCGCGCGCTTTCTTCGCGCTTCCCGGTCCG 1183

QY 299 GCTTCCCGCGGCGCGGCTCTGCTG---CATGCGGGGCGCCAGCTCCGGGCGCGCGCGA 355  
DB 1182 CCGGCGCTGCGCGGTGTCTTCTTCTTCCGCGCGCGCTTCTCCAGACCGGGTCCGCG 1123  
QY 356 GCTCATG 415  
DB 1122 GGTCCCGCGGCGGCGGTCTTCCGCGCGCTGCGCGCGCGCTTCCCGGAGCGTCCGTC 1063  
QY 416 CACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGC 458  
DB 1062 CCGGCGGTGCGGTGCGGAGAGCCCGTCTCCCGGTGCGG 1020

## RESULT 13

US-11-052-554A-529/c  
; Sequence 529, Application US/11052554A  
; Publication No. US20050288866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052,554A

PRIOR FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PatentIn version 3.3

SEQ ID NO 529

LENGTH: 3240

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis H37Rv

US-11-052-554A-529

Query Match 5.1%; Score 67; DB 12; Length 3240;

Best Local Similarity 46.3%; Pred. No. 2.8e-05;

Matches 220; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 1 CGACCGCGGTCTCGAGCGAAACCGATCTCTTGACTTGAATGAGGAGAGAGCGG 60  
DB 1645 CGGCACCTTTCGCGCGCGCGCGCGCGGTACCGGGCGCGCGCGGTGCGCGCGCGC 1586  
QY 61 CCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCTGGGAGAACTTACCGGCAAGCTCAGCCCC 120  
DB 1585 CGGTATATGCGCGCGCTTGGCGCGCGGTCCGCGCGCACCGCGCACCTTGACACG 1526  
QY 121 GCGCGGAGCGCGCGCGCGCGCGCGCTGCGAGCCATTTCGAGCGCACCGCGGCACTGCGG 180  
DB 1525 CCGCACCGCGCGCGCGCGCGCGCGCGCGCTGCGCACTTGTGCGCGTCCGCGCGCGCGG 1466  
QY 181 ACGCCCGCGGCGCTGCGAGGAGGCGCGGGGCGCGAGCGGAGCGCGGTCCGCGGAC 240  
DB 1465 TGCGCGCGCGCGCTCGGTGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCG 1406  
QY 241 TGAGCGCGCGCGCGCGCGGAACTTGGCGCGGAGCCGAGCGCGCGGAGCGGGGCGCGC 300  
DB 1405 CCGCGCGCGCGCGCGCGGTGCGGTGAGCTGAGAGGCTGCGCGCGCGCGCGCGGTGCGC 1346  
QY 301 CTCGCCCGCGCGCGCGCTTCTGCAATGCGGGGCGCGAGCTCCGAGGCGCGGCGGAGCGCC 360  
DB 1345 CCGCACCGCGCTTGGCGCGCGGTGCGAGGCGGTGAGCGCGCGCGCGCGCGCGCGCGAG 1286  
QY 361 CCGCTCATGACCG 420  
DB 1285 CCG 1226  
QY 421 CTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGAGCCGAAATGCTTC 475  
DB 1225 CCGGACTGGTGTGGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1171



RESULT 14  
US-11-052-554A-539

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; Sequence 539: Application US/11052554A
; Publication No. US20050288866A1
;
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30653/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 539
;
; LENGTH: 2196
;
; TYPE: DNA
;
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-539

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Query Match	5.0%;	Score 65.8;	DB 12;	Length 2196;
Best Local Similarity	50.4%;	Pred. No. 5.1e-05;		
Matches 213; Conservative	0;	Mismatches 207;	Indels 3;	Gaps 2;

[illegible]

RESULT 15  
US-11-121-086-2/c  
Severance ? Application re/111121086

Sequence #: US20050286459A1  
Publication No. US20050286459A1  
GENERAL INFORMATION: TIM S.  
APPLICANT: NIELSEN, KIRSTEN V.  
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
FILE REFERENCE: 09138.6000-00000  
CURRENT APPLICATION NUMBER: US/11/121, 086  
CURRENT FILING DATE: 2005-05-04  
PRIOR APPLICATION NUMBER: 60/567,570

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; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3.3
; SEQ ID NO. 2
; LENGTH: 191684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-2

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Query Match	5.0%;	Score 65.6;	DB 12;	Length 191684;
Best Local Similarity	51.0%;	Pred. No. 5.5e-05;		
Matches 207; Conservative	0;	Mismatches 194;	Indels 5;	Gaps 2;

Oy 55 AGGAGCGCGCGCGCGCGCGCGCGCGAGCGCGCTCGCTGGGAGAAAGCTAGCGGAGAGGCTC 114  
 Db 145265 AGGCGCTGCGCGAGAGCGCGAGTGGGCGCGCGCGGGGGCGGGTTCTTCGCGCCGAGACCCC 145206  
 Oy 115 AGCCCGCGCGCGAGCGCGCGCGCGCGCTGCGCAGCCATTTCGAGCGCCACCGCGGGCA 174  
 Db 145205 GCGCCCGCGCGCGCGCGCGCGCTCGAGAGTGTGAGAGGCGCGCGCGCGCGCGCGCGT 145146  
 Oy 175 CTGCGCGAGCGCCCC--GGGGCTGGCCGAGAGGAGCGCGGGGGGGCGAGCGAGCGGCGT 232  
 Db 145145 GCTGGGGGCGCGCGCGAGGAGGCGCTCTCGGGGAGGAGCGCGCTGTGGCGCCGCCCGCGGGC 145086  
 Oy 233 CGCGGCACTGAGCGCGCGCGCGCGCGCGCGGAACTTGAGCGCGGACCGCAGCGCGCGAGCG 292  
 Db 145085 TCCGGTGGCTCAGAGACGCGCTCAGCGGGGCGAGGCGCGGAGCGCGGCGTCCGCGGCG 145026  
 Oy 293 GGGCGCGGCT--CCCGCGCGCGCGCGCTCTGTCAGTCGAGGAGCCCGAGCTCCGGGCGCG 349  
 Db 145025 GCGCGCGCGCGCGCGCTCTCTCTCTCTCTCGCGCTCCGCGACTGAGCAGCGCGCGCG 144966  
 Oy 350 GCGGAGCGCGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 409  
 Db 144965 GCGCGAGCGAGCGCGCGCTCCGCGCGCGCTCCGCTCCGCGCGCGCGCGCGCGCGCGCTTGTCTC 144906  
 Oy 410 TCCATGACCGCGTTGATGGGGGTCAACAGCAGCAGCGCGCGCGCGCG 455  
 Db 144905 GGCATGTGCGCGCGCGCGTGGCGTGGCTGATTTACTTCGCGCGCGACG 144860

Search completed: February 28, 2006, 10:28:36  
Job time : 1733.47 secs

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